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(SAKA) OTSUKA PHARM CO LTD.	27-маr-1998; 98JP-0100467.	24-MAR-1999; 99WO-JP01512.		07-OCT-1999.	WO9950412-A1.		/label= oligomerisation_domain	Domain 353397	/label= DNA_binding_domain	Domain 142321		ain	Key Location/Qualifiers		Homo sapiens.	,	on; diagnosis	Human: p51; p53 related gene: cell proliferation: regulation: cancer:		Human p51 protein B.		07-TAN-2000 (first entry)		AAY45247;	AMITYJETT STANDALD; FIOLETH; OTT AM.	AAY4024/

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Matches 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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 SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI 600
                                                                                                         SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQ1EHY
                                                                                                                                                        GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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                                               SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 152-154; 163pp; Japanese
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                                                                                                                                                                                                          CC ell regulatory proteins (CRPs) termed the p63 family of coll regulatory proteins (CRPs) termed the p63 family of proteins, CC which demonstrate certain sequence identity to known tumour CC suppressor proteins p53 and p73. It has been observed that the CC intron-exon organisation is conserved between p73 and p53, and from CC known exon and intron sizes for these 2 genes, it was possible to CC identify now members of this gene family using a PCR-based strategy CC intron. The human p53 gene was localised to chromosomal position CC 3q27-29. At least 6 different isotypes exist. Splice variants CC differing at the C-terminus have been designated as alpha, beta and CR gamma forms, while p63 members differing in the N-terminus are CC designated as deltan and TA forms, where the deltan form lacks the CT transactivation domain. The present sequence represents human CC p63 isotype TAp63.alpha. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate of p63 expression CC differentiation, both benign and neoplastic. Deltan isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. CC cachexia) and neuronal differentiation and related degenerative cc disorders. p63 polypeptides (see AAV05953-64), polynucleotides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to cidentify compounds useful for treating disorders involving such
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                                                                                                                         Sequence
                                                                                                                                                                                 processes,
transgenic
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Pred. No. 2.4e-273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimera gene of the p53 of cancer, comprises a t
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                                                             SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 AA;
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Pred. No. 2.4e-273;
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                                                                                                                                                                                                                                                                                oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fritz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically defined disease with chromosomal aberration yielding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 352-354; 389pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                                                  Local
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                                                                                                                                                 641;
61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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                                                                                                                                                                  Similarity
                                                                               MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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                                                                                                                                                                                                                            641 AA;
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                                                                                                                                                                                                                                                                is the amino acid sequence of a human oncogenic protein
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Pred. No. 2.4e-273;
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30-DEC-1999;
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99US-0466396
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Pred. No. 5.1e-273;
0; Mismatches 1;
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                                                                                                                                                                                      CC protein (HEP)-90, or selectively treating cells expressing (II)
CC involving administering HEP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HEP)-90 (e.g.
CC protein isoform in a patient heterozygous for (II). The method is useful
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoletic disorder such as T or B cell
CC Iymphoma, chronic myeloid leukaemia (CML), APL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                         Matches
                                                                                                            Query Match
Best Local
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein or cellular protein isoforms (II) dependent on heat shock
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DB; ABS73328.
                                                                                                          Similarity
MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                    641
                                                                                       Conservative
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                                                                                 Score 3401; DB 23; Pred. No. 5.1e-273; 0; Mismatches 1;
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RESULT 6
ABG95128
ID ABG9
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ABG95128

standard;

Protein; 641 AA

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Length Indels

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considered with chromosomal aberrations yielding oncogenic fusion coll population, treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant careful protein or cellular protein isoforms (II) dependent on heat shock containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant careful for contein (HSP)-90, or selectively treating cells expressing (II) contein (HSP)-90, or selectively treating cells expressing (II) containing fusion concogenic fusion protein, treating cancerous cells containing fusion concogenic fusion protein, treating cancerous associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. ps3), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful containing a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemaia (CML), ALL, AML, NHL and CML, contained by a solid tumour such as papillary thyroid cortinoma, Eminy's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and containing sarcoma. The method is also useful for treating viral confections. This is the amino acid sequence of a human oncogenic protein. Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90 describes a method of treating 338-340; English genetically-defined disease

Sequence 641 AA;

Query Match

Local Similarity

640;

Conservative

99.98;

Score 3401; DB 23; Pred. No. 5.1e-273; 0; Mismatches 1;

Indels Length

Gaps

641; 0;

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Best Local S
Matches 640
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes isolated human lung carcinoma polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the patient of cancer in the patient. (I) and (II) are useful in the patient of the contaction of the cancer in the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang T,
McNeill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-2000; 2000US-0735705
07-MAY-2001; 2001US-0850716
28-JUN-2001; 2001US-0897778
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                            pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 328-329; 381pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-2001; 2001WO-US47576
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                                                                                                                                                                                     Local Similarity 99.1
les 640; Conservative
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                                                                       MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
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PD, Fanger N, Rette
, Watanabe Y, Peckh
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Retter MW, Durham M, Fo
Peckham DW, Cai F, Foy
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                                                                                                                                                                                  Score 3401; DB 23;
Pred. No. 5.1e-273;
0; Mismatches 1;
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Foy TM;
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15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
                   Wang T, Wang A, Skeiky YAW, Li
McNeill PD, Fanger N, Retter MW,
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02-AUG-2000;
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W. Marnerakis
                Kalos MD,
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Best Local Sim
Matches 640;
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                                                                                          SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHY
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                                                                    DAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 641
                                                                                                                                       SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVGFLARLGCSSCLDYFTTQGLTTIYQIEHY
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immune response -
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Best Local
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
                                                                                                                                                                                                                                                                       This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypurolectides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lung can
vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 250-253;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide protein is used for d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                                                                                                                      Sequence
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                                                                                                              Fan
                                                                  ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                       PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                  PQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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261pp;

English

and monitoring progress;

ic portion of progression of

of Of

lung lung

cancer tumor

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Score 3397; DB 21; Pred. No. 1.2e-272; 0; Mismatches 1;

Indels Length

Gaps

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279 240 219

180 159 120 99

680; 0

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RESULT 11
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             This invention describes a novel KET-encoding nucleic acid (I) and its fragments, variants and mutants which has anticancer activity. (I) encodes a protein, (II), involved in control of the cell cycle and apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to detect (I) in biological samples, specifically anglogenic tumor tissue, including (I) sequences that have a homozygotic deletion and (b) to detect presence or absence of human chromosome 3q27 or murine chromosome los or their fragments, by hybridization. Also, (I) is used as a tumor
                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                            New KET-encoding nucleic acid treatment of tumors -
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family; angiogenic; cytotoxic; cancer; human.
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DAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                             SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI
                                                                                                               SPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTTIYQIEHY
                                                                                                                                                               GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                                                                                                FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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                                                                                                   SPTQALPPPLSMPSTSQCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHY
                                                                                                                                                   GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 3397; I
Pred. No. 1.26
0; Mismatches
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es 1;
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ABP61913 standard; Protein; 680 B

ABP61913;

07-OCT-2002 (first entry)

lung cancer associated protein sequence SEQ IJ NO:342

Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine

WO200247534-A2

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                                                                                                                                                                                                                                                                                                                                                                                                    Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes isolated human lung carcinoma compositions of polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the obtaining a biological sample from the patient, contacting the amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer.

AB092145 to AB092486 and ABP61866 to ABP6192 represent sequences used in the exemplification of the present invention.
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Best Local S
Matches 640
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McNeill PD,
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07-MAY-2001;
28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 331-333; 381pp;
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PD, Fanger
), Watanabe
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LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSY
                                                           FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                         ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                                                    SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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                                                                                                                           ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
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; 2001US-0850716.
; 2001US-0897778.
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er N, Retter MW,
be Y, Peckham DW,
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, Durham M, Fanger
W, Cai F, Foy TM;
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L.2e-272;
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02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
                                                                       The present invention describes human lung tumour proteins. Human lun tumour proteins and polynucleotides have cytostatic and immunostimula activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, tumour proteins, or antigen presenting cells that express the lung tumour proteins, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer stimulating an immune response. ABIA9300 to ABIA9300 and ABB74946 to ABB7570 represent sequences used in the exemplification of the present proteins.
                                                                                                                                                                                                                                                                                                                                                            Wang T,
McNeill
                                Sequence
                                                                                                                                                                                                                                                  Polynucleotides encoding lung lung cancer or stimulating an
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07-MAY-2001;
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DB; ABL49250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lung tumour;
                                                                                                                                                                                                                                                                                                                                           Wang.A, Skeiky YAW, PD, Fanger N, Retter TS,. Carter D, Watana
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2000US-0630940.
; 2000US-0643597.
; 2000US-0662786.
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; 2000US-0735705.
; 2001US-0850716.
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Retter MW,
Watanabe Y,
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                                                                                                                                                                                                                                                      immune
                                                                                                                                                                                                                                                                    tumor polypeptides,
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, Marnerakis M,
Y, Peckham DW;
                                                                                                                                                                                                                                                      response
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Fanger GI
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Query

Match

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                          29-MAY-1998;
15-OCT-1997;
                                                                                       02-OCT-1998;
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                              Cell regulatory protein; p63; hu-deltaNp63 gamma; human;
                                                                                                                                                                                                                                                                                                                                     Human cell regulatory protein p63, isoform deltaNp63 gamma
                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY05958
                                                                                                                                                                        WO9919357-A2
                                                                                                                                                                                                                                                         proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour suppressor; cell cycle control; apoptosis bliferation; cell differentiation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAVRFTLRQTISFPFRDEWINDENFDMDARRNKQQRIKEEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSSETRGERVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                          98US-0087216.
97US-0062076.
                                                                                       98WO-US21992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isotypes exist. Splice variants differing at the C-terminus have been designated as alpha, beta and campana forms, while p63 members differing in the N-terminus are designated as deltaN and Ta forms, where the deltaN form lacks the transactivation domain. The present's equence represents human companies that the noterminus are p63 isotype hu-deltaNp63 gamma. p63 was detected in a variety p63 isotype hu-deltaNp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous afferentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. Cessatives towards transactivation by p53 and p63. Cessatives towards transactivation by p53 and p63. Cessatives towards transactivation and related degenerative characters. p63 polypeptides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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                                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 98.1
29; Conservative
LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLLQKQTSIQSPSSY
                                                                                     FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                   ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSQSTQTSEFLSPEVFQHIWDFLEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                              PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                               FEARICACPGRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                             ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 concerns the discovery of a new family of ins (CRPs) termed the p63 family of proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3353; DB 20;
Pred. No. 5.3e-269;
8; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. treatment
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                                                    This invention describes a novel KET-encoding nucleic acid (I) and its fragments, variants and mutants which has anticancer activity. (I) encodes a protein, (II), involved in control of the cell cycle and apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to detect (II) in biological samples, specifically angiogenic tumor tissue, including (I) sequences that have a homozygotic deletion and (b) to detect presence or absence of human chromosome 3q27 or murine chromosome 16, or their fragments, by hybridization. Also, (I) is used as a tumor suppressor, particularly in tumors where an alteration in the wild-type p53 allele has not been identified. (I) and (II) may also be used for developing cancer. This sequence represents the rat KET protein described in the activation of the content of the 
    Sequence
                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                        New KET-encoding nucleic acid treatment of tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-1998;
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                                           method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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    089
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angiogenic; cytotoxic; cancer; rat.
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Query Match Best Local S Matches 629

Similarity

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	Sequence 2, Appli	Sequence 32, Appl	Sequence 7, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 26, Appl	Sequence 25, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 27, Appl	Sequence 2, Appli	Sequence 20, Appl	Sequence 3, Appli

ALIGNMENTS

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APPLICANT: Wang, Alj...

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

"MURRER OF SEQ ID NOS: 369
                                                                                                                                                                                                                                                                                                                                                                       ; SOFTWARE: FastSEQ for Wi
SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-339
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US-09-643-597-339
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Best Local Similarity
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Fanger, Gary F
Li, Samuel X.
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Fan, Liqun
Kalos, Michael D.
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APPLICANT: KAIOS, MICHAEL D.

APPLICANT: HOSKEN, NANCY A.

APPLICANT: HOSKEN, NANCY A.

APPLICANT: FANGEY, GATY R.

APPLICANT: FANGEY, GATY R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C8

CURRENT APPLICATION NUMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 350

SOFTWARE: FASTSEQ for Windows Version 3.0

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Best Local Sim
Matches 640;
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                                                                                     SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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US-09-606-421B-339
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SOFTWARE: FastSEQ for Windows Version
SEO ID NO 339
LENGTH: 641
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APPLICANT: Wang, Aljun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C9

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28
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APPLICANT:
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Pred. No. 2.9e-304;
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US-09-643-597-342; Sequence 342, App; Patent No. 642607
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CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
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TYPE: PRT
ORGANISM: Homo sapiens
-09-643-597-342
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Fanger, Gary R.
Li, Samuel X.
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LENGTH: 680
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Best Local
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                                                                                                                                           Matches
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Garty R.
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows
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                                            DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
                                                                                   MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Fan, Liqun
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                                                                                                                                           Conservative
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                                                                                                                                        Score 3397; DB 4;
Pred. No. 7.4e-304;
0; Mismatches 1;
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OF LUNG CANCER
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APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
US-09-606-421B-342
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APPLICANT:
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5. 6531315
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Fanger, Gary R.
Li, Samuel X.
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Bangur, Chaitanya S.
                                                                                        Conservative
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                                                                                       Score 3397; D
Pred. No. 7.4e
0; Mismatches
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; ORGANISM: Homo
US-09-643-597-338
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US-09-643-597-338
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SEQ ID NO 338
LENGTH: 586
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Best Local S
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APPLICANT: Wang, I
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APPLICANT:
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                                                                                                                                                                        APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIACNOSIS OF LUNG CAN
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
                                                                                                                                                 CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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\verb"PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN"
                                                                                                                                        FastSEQ for Windows Version
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Fan, Liqun
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Li, Samuel X.
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Pred. No. 6.9e
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAPILLA FERRENCE: 20121.45C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
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US-09-542-615A-338
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Best Local (
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                                                                                                                                                          ORGANISM: Homo sapiens
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 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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                                                                                   Score 3016; DB 4;
Pred. No. 6.9e-269;
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SOFTWARE: FastSEQ for W
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-606-421B-338
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US-09-606-421B-338
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitan
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 338, Application US/09606421B Patent No. 6531315
                                                                                                  Matches
                                                                                                              Query Match
Best Local :
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.45509

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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                                                                                                               Similarity
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Fanger, Gary R.
Li, Samuel X.
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Pred. No. 6.9e-269;
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APPLICANT: Skekky, Yasir A.W.
APPLICANT: Skekky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeili, Patricia D.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Window-
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo s
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Pred. No. 3e-268;
2; Mismatches
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APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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GENERAL INFORMATION:
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Pred. No. 3e-268;
2; Mismatches
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Kancy A.
APPLICANT: Hosken, Kancy A.
APPLICANT: Hosken, Kancy A.
APPLICANT: Franger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455CB
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
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Sequence 152, Application US/09542615A
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                                      PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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99.3%;
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Pred. No. 3e-268;
2; Mismatches
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APPLICANT: Li, Samuel X.
APPLICANT: Mang, Aijun
APPLICANT: Wang, Aijun
TITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitan
APPLICANT: Hosken, Nancy
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Pred. No. 3e-268;
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: L, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
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Best Local S
Matches 511
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Patent No. 642607
GENERAL INFORMATI
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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                       GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
PQGAVIRAMPYYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYYEDP
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Fan, Ligun
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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FO

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA

FILE REFERENCE: 210121.455C8

CURRENT APPLICATION NUMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEO ID NOS: 350

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 344

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US-09-542-615A-344
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US-09-542-615A-344
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GENERAL INFORMATION:
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Best Local
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Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S.
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                                                                                           PQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                       MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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; Pred. No. 6.5e-242;
0; Mismatches 0;
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Search completed: August 7, 2003, 09:54:49 Job time : 19.6828 secs	481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511	481 SPTQALPPPLSMPSTSHCTPPPPPYPTDCSIV 511	421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL 480	421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL 480	361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY 420	361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSY 420	301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 7, 2003, 09:46:34; Search time 27.3662 Seconds Run on:

(without alignments) 2781.719 Million cell updates/sec

Title: Perfect score:

US-09-538-106-13 3405 1 MSQSTQTNEFLSPEVFQHIW......FNFDMDARRNKQQRIKEEGE 641 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

451899 seqs, 118759770 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA: Database

/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata///pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:

CIMMARTEC

	Description	Sequence 339, App	Sequence 339, App	Sequence 339, App	Sequence 342, App	Sequence 342, App	Sequence 342, App	Sequence 338, App	Sequence 338, App	Sequence 338, App	Sequence 152, App	Sequence 152, App	Sequence 152, App	Sequence 152, App	Sequence 344, App	Sequence 344, App
SUMMARIES	QI	US-09-735-705-339	US-09-850-716A-339	US-09-897-778-339	US-09-735-705-342	US-09-850-716A-342	US-09-897-778-342	US-09-735-705-338	US-09-850-716A-338	US-09-897-778-338	US-09-735-705-152	US-09-850-716A-152	US-09-897-778-152	US-09-466-396A-152	US-09-735-705-344	US-09-850-716A-344
	DB	6	10	10	σ	10	10	σ	10	10	σ	10	10	11	6	10
	å Query Match Length DB	641	641	641	680	680	680	586	586	586	586	586	586	586	516	516
	Query Match	6.66	99.9	99.9	99.8	8.66	98.8	88.6	98.6	88.6	88.4	88.4	88.4	88.4	79.9	79.9
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Sequence 344, App Sequence 343, App Sequence 343, App Sequence 340, Appl Sequence 340, Appl Sequence 341, Appl Sequence 341, Appl Sequence 341, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 9, Appl Sequence 9, Appl Sequence 9, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 3, Appl Sequence 4, Appl Sequence 4, Appl Sequence 6, Appl Sequence 3, Appl Sequence 3	
US-09-897-778-344 US-09-735-705-343 US-09-850-716A-343 US-09-880-778-343 US-10-274-874-19 US-09-897-778-343 US-09-897-778-340 US-09-897-778-340 US-09-897-778-341 US-09-897-778-341 US-09-735-705-341 US-09-735-705-341 US-09-735-705-341 US-09-735-705-341 US-09-735-705-341 US-09-735-705-341 US-09-735-705-341 US-10-15-059-3 US-09-735-384-3 US-09-736-905-3 US-09-860-211-9 US-09-860-211-9 US-09-860-211-9 US-10-10-10-290-2 US-10-10-10-290-2 US-10-10-10-290-2 US-10-10-10-290-3 US-10-10-10-290-3 US-10-10-290-3 US-10-10-290-3 US-10-10-290-3 US-10-10-290-3 US-10-10-290-3 US-10-10-290-3	
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ALIGNMENTS

RESULT 1

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Length 641;
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APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Eager, Neil
TTILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DISGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
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Pred. No. 4.5e-273;
0; Mismatches 1;
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Sequence 339, Application US/09735705 Patent No. US20020052329A1
                                                                                          Kalos, Michael D. Bangur, Chaitanya S Hosken, Nancy Fanger, Gary R. Li, Samuel X. Wang, Aljun Skelky, Yasir A.W.
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99.8%;
                                                          Wang, Tongtong
Fan, Liqun
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US-09-735-705-339
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                                      GENERAL INFORMATION:
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Best Local Simi
Matches 640;
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SEQ ID NO 339
LENGTH: 641
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Sequence 339, Application US/09897778 Patent No. US20020147143A1
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APPLICANT: Marnerakis, Margarita
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APPLICANT: Kalos, Michael D.
APPLICANT: Racelly. Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILLE REFERENCE: 210121.455615
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
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Pred. No. 4.5e-273;
0; Mismatches 1;
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Pred. No. 4.5e-273;
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APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHO.
FILE OF INVENTION: AND DIAGNOSIS OF LUNG (
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
                                       ; ORGANISM: Homo US-09-735-705-342
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Henderson, Robert A.
McNeill, Patricia D.
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3397; DB 9;
No. 1.1e-272;
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                                                                                         CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Retter, Marc W.
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                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C15
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TYPE: PRT
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                99.8%;
 Score 3397; DB 10;
Pred. No. 1.1e-272;
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US-09-897-778-342
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                                        ; ORGANISM: Homo sapiens US-09-897-778-342
                                                                                            APPLICANT: PECKHAM, DAVID W.

APPLICANT: PENDEY, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 342
                                                                                                                                                                                                                                         APPLICANT: Wang,
APPLICANT: Marnel
APPLICANT: Fange
APPLICANT: Vedvic
APPLICANT: Carte
APPLICANT: Watan
APPLICANT: Hende
                                                                                                                                                                                                                                                                                                                                          Sequence 342, Application US/09897778 Patent No. US20020147143A1 GENERAL INFORMATION:
 Best Local Similarity
              Query Match
                                                                    LENGTH: 680
TYPE: PRT
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Carter, Darrick
Watanabe, Yoshihiro
Henderson, Robert A.
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Score 3397;
Pred. No. 1
 1.1e-272;
              Length 680;
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       DAVRETLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 641
                            {\tt FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE}
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DAVRETLROTISFPPRDEWNDFNFDMDARRNKOORIKEEGE
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RESULT 7
US-09-735-705-338
SOFTWARE:
SEQ ID NO 3
LENGTH: 5
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APPLICANT: Wang, T
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APPLICANT:
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APPLICANT:
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                                              CURRENT APPLICATION NUMBER: US/0 CURRENT FILING DATE: 2000-12-12 NUMBER OF SEQ ID NOS: 419
                                                                                       TITLE OF INVENTION: COMPOSITIONS AT TITLE OF INVENTION: AND DIAGNOSIS FILE REFERENCE: 210121.455C14
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                                           NUMBER OF SEQ ID
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 · 338
586
                              FastSEQ for Windows Version
                                                                                                                                       Fanger, Neil
                                                                                                                                                  McNeill, Patricia D.
                                                                                                                                                                                  Skeiky, Yasir A.W.
                                                                                                                                                                                                    Wang,
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Li, Samuel X.
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Bangur, Chaitanya
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                                                                                                       COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                          US/09/735,
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GENERAL INFORMATION:

APPLICANT: Kalos, Michael D.

APPLICANT: McNeill, Patricia D.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C15

CURRENT APPLICATION UNUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 338

LENGTH: 586
                                                       ; TYPE: PRT
; ORGANISM: Homo
US-09-850-716A-338
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  Matches 569; Conserv
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    Conservative
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              99.5%;
 Score 3016; DB 10;
Pred. No. 3.1e-241;
1; Mismatches 2;
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Pred. No. 3.1e-241;
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0;
                                                                  CURRENT APPLICATION NUMBER: US/09/897,778.
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 338
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-338
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US-09-897-778-338
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              Query Match
Best Local Similarity
Matches 569; Conserva
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Franger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
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                                                                                                                                                                                                                                                                Carter, Darrick
Watanabe, Yoshihiro
Henderson, Robert A.
                                                                                                                                                                                                                                                                                                          Fanger, Gary R. Vedvick, Thomas
                                                                                                                                                                                                                                                                                                                                      Marnerakis, Margarita
              Conservative
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                                                                                                                                                                                                                                                                                                          Thomas S.
                           99.5%;
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             Score 3016; DB 10;
Pred. No. 3.1e-241;
1; Mismatches 2;
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Length

586; 0;

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TITLE OF INVENTION: COMPOSITIONS AND METHOD
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG OF FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PAT
ORGANISM: Homo sapien
US-09-735-705-152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
    Best Local Similarity
                       Query Match
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Henderson, Robert A.
McNeill, Patricia D.
Fanger, Neil
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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Skeiky, Yas:
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Fan, Liqun
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      88.4%;
99.3%;
    Score
Pred.
    3009;
No. 1.
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LUNG CANCER
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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Metter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 2101.21.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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US-09-850-716A-152
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pred. No. 1.2e-240;
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
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SEQ ID NO 152
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APPLICANT: Marner
APPLICANT: Fanger
APPLICANT: Vedvic
APPLICANT: Watans
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                                                PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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Vedvick, Thomas S.
Carter, Darrick
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Marnerakis, Margarita
                                                                                   Conservative
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99.38;
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No. 1
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APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOUNDS AND METHODS FOI

TITLE OF INVENTION: . DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C4
                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 152
LENGTH: 586
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                                                                                                                                                                                         Matches
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Pred. No. 1.2e-240;
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LENGTH: 516
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT:
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                                                                                    DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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Fanger,
Li, Samu
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TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
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ORGANISM: Homo
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                                                                                   | ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                      MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                          FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                          PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                    SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                                                                                                 SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                             PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPTQALPPPLSMPSTSHCTPPPPPYPTDCSIV 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL 480
             FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTQALPPPLSMPSTSHCTPPPPPPTDCSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLLQKQTSIQSPSSY
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                                                                    ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09850716A
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                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                       Score 2722; DB 10;
Pred. No. 5.8e-217;
0; Mismatches 0;
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Gaps

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Result
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Maximum DB seq length: 2000000000
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                            714.5
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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3405
1 MSQSTQTNEELSPEVFQHIW.....FNFDMDARRNKQQRIKEEGE
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Query
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Listing first 45 summaries
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1520
901
2579
628
1062
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1819
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921
628
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               JH063

S02193

S02194

S02164

S02164

S02164

JH0633

DNHU53

DNHU53

JC6173

S06594

S06594

S06594

S06594

S066794

S066796

T146226

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S06736

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  T40290
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C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Pate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: JH0631
R.de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A.Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A.; Reference number: JH0631; MUID:92210006; PMID:1339362
A.; Accession: JH0631
A.; Molecule type: mRNA
A.; Residues: 1-396 <DEF>
A.; Accession: JH0631
A.; Residues: 1-396 <DEF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829
A;Experimental source: liver
G;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive;Superfamily: cellular tumor antigen p53
C;Reywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phc G;Reywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phc F;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphoryi-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
JH0631
cellular tumor antigen p53 - rainbow trout
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ALIGNMENTS

Ral Similarity 45.4%; Pred. No. 6.1e-51; 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10 11 LSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70 : : : : : : : : : : : : : : :	Qy 361 Db 327	Qy 309 рь 267	Qy 249 Db 207	Qy 189 Db 148	.Qy 12 .Db 8	Qy 7 Db 4	Qy 1 Db 1	Query Matc Best Local Matches 1
	1 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399 		9 VPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGVLGRRGFEARICAC 308 :	9 MPVYKKAEHVTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGROSVL 248 	9 NTDYPGDHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA 	1 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPS-STFDALS-PSPAIPS 128 	1 LSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70 	Query Match 24.9%; SCOTE 84.75; DB 1; Length 396; Best Local Similarity 45.4%; Pred. No. 6.1e-51; Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;

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cellular tumor antigen p53 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Nonopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29376; S61531; S72313; I51639
R;Soussi, T.; de Fromentel, C.C.; Mechall, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a A;Reference number: A29376; MUID:88143684; PMID:2830576
A;Molecule type: mRNA
A;Residues: 1-363 <SOU>
A;Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962
R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A;Title: Overexpression of wild-type p53 interferes with normal development in X
A;Reference number: I51639; MUID:94134403; PMID:8302570
A;Accession: S61531
A;Molecule type: mRNA
A;Residues: 1-293,295-363 <HOE>
A;Residues: 1-293,295-363 <HOE>
A;Reference number: S72313
A;Accession: S72313
A;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; C;Keywords: apoptosis; cell division (Cys, His, Cys, Cys) #status predicted F;150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
RESULT
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A; Cross-references: EMBL: X77546; NID: g4685
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Best Local
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                                                                                                                                               R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI
                                                                                                                                                                                                                                                             RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR 354
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                                                                                                              LVVVDDDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV
                                                                                                                                                                                                                               RRCFEVRVCACPGRDRRTEEDNYTKKRGLKPSGK---
                                                                                                                                                                                                                                                                                                                                             EDVNSGRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTIITLETPQGLLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYV
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Pred. No. 3.7e-46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <HOW>.513; PIDN:CAA54672.1;
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RESULT 4
S51648
                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-386 <DEQ>
                                                                                                                                                                                                                                                                                                     cellular tumor antigen p53 - bovine N;Alternate names: tumor-suppressor protein C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Se C;Accession: S51648 R;Dequiedt, F; Willens, L.; Burny, A.; Kett R;Dequiedt, F; Willens, L.; Burny, A.; Kett R;Dequiedt, F; Willens, L.; Burny, A.; Kett R;Dequiedt, F; Willens, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A;Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear once A;Reference number: S02193; MUID:89083584; PMID:3060861
A;Recession: S02193
A;Accession: S02193
A;Coession: S02193
A;Coession: S02193
A;Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741
A;Residues: 1-367 <SOUV
A;Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleicted F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                       A;Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333 C;Superfamily: cellular tumor antigen p53 C;Reywords: apoptosis; cell division control; DNA binding; homotetramer; pl C;Reywords: apoptosis; cell division control; DNA binding; homotetramer; pl F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
                                                                                                                                                                                                       A; Accession: S51648
                                                                                                                                                                                                                             A; Reference number:
                                                                                                                                                                                                                                                             A; Description:
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S02193
R;Soussi, T; Begue, A.; Kress, M.; Stehelin, D.; May, P.
F;385/Binding
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Best Local :
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site: phosphoryl-RNA (Ser) (covalent) #status predicted
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44.6%; Pred. No. 2.9e-45;
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                                                                                                                                                                                                                                                          Burny, A.; Kettmann, R. ibrary, September 1994 quence of the ovine p53
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Score

740;

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Length

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992 C;Genetics: A;Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph F;174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted Query Match Best Local Similarity 38.3%; pred. No. 3.5e-43; Matches 171; Conservative 72; Mismatches 134; Indels 70; Gaps 13; Matches 171; Conservative 72; Mismatches 134; Indels 70; Gaps 13; A SQSDMSTELPISQETFSCLWKLLPPDDILPTANTGSPNSME	Qy 399 QQQQH-QHLLQKQTSIQSPSSYGNSSPPLNK 429 ::	Best Local Similarity 45.8%; Pred. No. 1.5e-43; Matches 152; Conservative 57; Mismatches 94; Indels 29; Gaps 8; Qy 108 SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTEL 159
Db 14 LSQETESDLWKLL	SULT 6 10633 Species: Me Alternate n Species: Me Date: 10-Se Accession: Legros, Y.; ne 112, 24; ne 112, 24; Title: The Reference n Accession: Cross-refer Experimenta Genetics: Genetics: 179,182,241 395/Binding Ouery Matches Olossion: Ol	Db 92 SSSVPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSISLNKLFCQLAKTCPVQLWVTSTP 149 Qy 181 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-TAPPSHLIRVEGNSHAQYVED 239 1

L.V.

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A:Title: Characterization of the human p53 gene.
A:Title: Characterization of the human p53 gene.
A:Reference number: A25224; MUID:87064416; PMID:2946935
A:Reference number: A25224
A:Reference number: DIAA
A:References: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; PIR
A:Gross references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; PIR
A:Residues: 1-393 < LAM>
A:Residues: Georgiev, G.P.
Gene 70, 245-252, 1988
A:Title: A variation in the structure of the protein-coding region of the human p53 gene
A:Reference number: J70436; MUID:89108008; PMID:2905688
A:Reference number: J70436; MUID:89108008; PMID:2905688
A:Reference number: J70436; MUID:89108008; PMID:2905688
A:Rocession: A43073
A:Molecule type: DNA
A:Residues: 1-393 < BUC1>
A:Rocession: J70436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Isolation and characterization of a human p53 cDNA clone: expres A;Reference number: $42669; MUID:85126934; pMID:6396087 A;Accession: $42669
A;Accession: $42669
A;Molecule type: mRNA
A;Residues: 101-393 <MKI1>
A;Cross-references: EMBL:X01405; NID:g35215; pIDN:CAA25652.1; pID:g64224
R;Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
A;Title: Human p53 cellular tumor antigen: cDNA sequence and expression A;Reference number: A22837; MUID:85230577; pMID:4006916
A;Recession: A22837
A;Molecule type: mRNA
A;Residues: 1-71, 'P',73-393 <ZAK>
A;Residues: 1-71, 'P',73-393 <ZAK>
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 1-71, 'p', 73-272,'H',274-393 <HAR>
A;Residues: 1-71, 'p', 73-272,'H',274-393 <HAR>
A;Cross-references: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
A;Experimental source: clone pR4-2, cell line A431
R;Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.;
MO1. Cell. Biol. 6, 4650-4656, Prokocimer, M.; Wolf, D.; Arai, N.;
A;Title: Molecular basis for heterogeneity of the human p53 protein.
A;Reference number: A93086; MUID:87089826; PMID:3025664
                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E. Mol. Cell. Biol. 5, 1601-1610, 1985
Mol. Cell. Biol. 5, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for huma A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
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Cell. Biol. 6, 1379-1385, 1986
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A; Residues: 1-78, 'T', 80-393 <HAR1>
A; Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A; Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A; Accession: B25397
                                                                                                                                                                     A;Status: LINE MRNA
A;Molecule type: mRNA
A;Residues: 1-247,'Q',249-393 <F08>
N:Residues: 1-247,'NI
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-247,'Q',249-393 <F06>
A;Residues: 1-247,'Q',249-393 <F06>
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A;Molecule type: mRNA
A;Residues: 1-245,'T',247-393 <F04>
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A;Molecule type: mRNA
A;Residues: 1-192,'R',194-393 <F02>
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A; Residues: 1-199, 'LLISILSEWKEICVWSIMMTETLEDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA'
A; Residues: 1-199, 'LLISILSEWKEICVWSIMMTETLEDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA'
A; Rocossion of a C nucleotlide causes a frameshift at position 566
A; Accession: 138083
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R;Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.
EMBO J. 10, 2879-2887, 1991
A;Title: p53 is frequently mutated in Burkitt's lymphoma
A;Reference number: I38082; MUID:92007731; PMID:1915267
A;Accession: I38082
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A; Residues: 66-71,'P',73-79 <MKI2>
A; Experimental source: clone lambda C113
A; Note: 72-Cys was also found, and appears
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A;Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R;Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-71, 'P',
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A; Residues: 1-236, 'I', 238-393 <F05>
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A; Accession: 138085
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A; Residues: 66-79 < MKI3>
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                                    A; Molecule type: mRNA
A; Residues: 1-71, 'P', 7
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A; Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
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                                                                                                                         Status: translated from GB/EMBL/DDBJ
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        EMBL: X60018; NID: 9506448;
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EMBL:X60015; NID:g506442;
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                                            73-162, 'H', 164-393 <F09>
                                                                                                                                                                                              NID:g506446;
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PMID:3547088
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            PIDN:CAA42633.1;
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A;Title: p53 gene mutations in gastric cancer metastases and in gastric cance A;Reference number: A44905; MUID:92034678; PMID:1933850
A;Reference number: A44905; MUID:92034678; PMID:1933850
A;Recession: A44905
A;Rocession: A44905
A;Rocession: GB:S63157; NID:9237829; PIDN:AAB20140.1; PID:9237830
A;Rote: references: GB:S63157; NID:9237829; PIDN:AAB20140.1; PID:9237830
A;Rote: sequence extracted from NCBI backbone (NCBIN:63157, NCBIP:63158)
A;Rote: mutation from a liver metastasis of a gastric cancer
R;Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 6, 1067-1071, 1991
A;Title: Use of the single strand conformation polymorphism technique and PCI
A;Reference number: I58354; MUID:91296386; PMID:1648702
A;Reference number: I58354; MUID:91296386; PMID:1648702
A;Reference number: I58354; MUID:91296386; PMID:1648702
A;Reference number: GB:S41969; NID:9167931; PIDN:AAB19324.1; PID:9232814
A;Rocession: I78850
A;Cross-references: GB:S41969; NID:91679931; PIDN:AAB19324.1; PID:9232814
A;Residues: 274-277, 'W', 249-252 <HENI>
A;Residues: 274-277, 'S', 279-282 <HENI>
A;Cross-references: GB:S41977, NID:91678032, DIDN:AAB19324.1; PID:9232814
A;Residues: 274-277, 'S', 279-282 <HENI>
A;Cross-references: GB:S41977, NID:91678032, DIDN:AAB19324.1; PID:9232814
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Mol. Genet. 249, 425-431, 1995

A; Title: Mapping of linear epitopes recognized by monoclonal antibodies with A; Reference number: S60151; MUID:96133682; PMID:8552047

A; Accession: S60153

A; Molecule type: DNA
A; Residues: 3-44
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A;Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1; PID:g232816
R;Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A;Title: Alternative splicing of the p53 tumor suppressor gene in the Mol
A;Reference number: I52681; MUID:94036762; PMID:8221626
A;Accession: I52681
A;Scatus: translated from GB/EMBL/DDBJ
A;Scatus: translated from GB/EMBL/DDBJ
A;Scatus: translated from GB/EMBL/DDBJ
A;Gross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A;Note: mutant sequence with altered splicing and termination expressed in R;Petersen, G; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
Loop Company 
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J. Biol. Chem. 264, 18019-18023, 1989
A;Title: Nuclear and nucleolar target
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A;Cross-references: EMBL:X60019; NID:9:
A;Accession: I38092
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-253, 'D',255-393 <F11>
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A; Residues: 1-393 <FUT>
A; Cross-references: EMB
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A; Status: translated from GB/1
A; Molecule type: mRNA
A; Residues: 1-212,'Q',214-393
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A; Status: translate
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51, .
                                                                                                                                                                                             163;
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                                                                                     LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70
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L, 5800-5805, 1991
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la, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi,
                                                                                                                                                                                                                         21.18; 38.48;
                                                                                                                                                                                                                                                                                                                                                              targeting sequences of c-erb-A, c-myb,
                                                                                                                                                                               Score 718; DB 1;
Pred. No. 5.2e-42;
69; Mismatches 132;
-NNVLSPLPSQAMDDLMLSPDDIEQWFTE--DP---
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A; Molecule type: mRNA
A; Residues: I-159, 'H',161-167, 'G',169-233, 'I',235-390 <ZAK>
A; Residues: I-159, 'H',161-167, 'G',169-233, 'I',235-390 <ZAK>
A; Cross-references: GB:X01237; GB:K01700; NID:g55575
R; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Sh
Mol. Cell. Biol. 6, 3232-329, 1986
A; Title: Immunologically distinct p53 molecules generated b;
A; Reference number: S38822; MUID:87064640; PMID:3023970
A; Accession: S38822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular tumor antigen p53 - mouse N;Alternate names: oncoprotein p53 C;Species: Mus musculus (house mouse) C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000 C;Accession: A22739; S06336; A02664; S38823; S480014; I48703 R;Beienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M. EMBO J. 3, 2179-2183, 1984 A;Title: Analysis of the gene coding for the murine cellular tumour antigen A;Accession: A22739; MUID:85027173; PMID:6092064 A;Accession: A22739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioorg. Khim. 13, 1691-1694, 1987
A; Title: Primary structure of DNA complementary to murine A; Reference number: S06336; MUID:88221682; PMID:3329909
A; Accession: S06336
                                                                                                                                                                                                                                                                                                                                                              Nature 306, 594-597, 1983
A;Title: A single gene and a pseudogene for the cellular A;Reference number: A02684; MUID:84068204; PMID:6646235
A;Accession: A02684
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                                          A; Molecule type: mRNA
A; Residues: 1-167,'G',169-233,'I',235-390
                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-390 < ARA1>
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A; Residues: 1-13
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                     A;Cross-references:
                                                                                            A; Accession: S38823
                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Zakut-Houri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Chumakov, P.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-134,'V',136-390 <BIE>
A;Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-134,'V',136-390 <CHU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTITLEDSSGNLLGRNSFEVRVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAMAIYKQSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.; Oren, M.; Bienz, B.; Lavie, V.; Hazum,
EMBL: M13873
D.; Yokota, K.;
                                                                                                                EMBL:M13872;
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                                                                                                           NID: g200198;
Wolf, D.; Brill,
                                               <ARA2>
                                                                                                                PIDN: AAA39881.1;
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Shohat,
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                                                                                                             PID:g200199
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  Rotter,
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-47, 78, 49-78, 70W, 82-390 <RES>
A; Residues: 1-47, 78, 49-78, 70W, 82-390 <RES>
A; Cross-references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
C; Comment: This DNA-binding protein plays an essential role in the regulation of C; Comment: The tetramer association region may exhibit a beta-turn, beta-sheet, b C; Superfamily: cellular tumor antigen p53
C; Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphop F; 1-44/Domain: transcription activation #status predicted <TRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;313-319/Region: nuclear location signal
F;319-357/Region: tetramer association
F;319-357/Region: tetramer association
F;79,12-18,23-37/Binding site: phosphate (Ser) (covalent) #status predicted
F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F;389/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
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A;Title: Cloning and expression analysis of full length A;Reference number: 148703; MUID:84272240; PMID:6379601
A;Accession: 148703
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A; Reference number: S4
A; Accession: S40014
A; Accession: ype: mRNA
A; Molecule type: mRNA
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Best Local
371
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                                                                 QQQQQQHQHLLQKQTSIQS
                                                                                                                                       PQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---AHATEESGDSRAHSSYLKTKK
                                                                                                                                                                                                                                                                       SSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPELPPGSAKRALPTCT---SASP
                                                                                                                                                                                                                                                                                                                                                                                                                  NLYPEYLEDRQTFRHSVVVPYEPPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLED
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38.0%;
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Pred. No. 6e-42;
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III
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A;Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphor A;Reference number: S06594; MUID:90045967; PMID:2530498
A;Recession: S06594
A;Molecule type: mRNA
A;Residues: 1-393 <RIG>
A;Cross references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetrammer; nuc F:176,179,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellular tumor antigen p53 - green monkey
(;Specias: Cercopithecus aethiops (green monkey, grivet)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S06594
R;Rigaudy, P.; Eckhart, W.
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                                                                                  ACPGRDRRTEEENFRKKGEPCHELPPGSTKRALPNNT----SSSPQPKKKPLDGEYFTLQ
                                                                                                           ACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDELLYLP
                                                                                                                                                                        VVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVC
                                                                                                                                                                                                               VLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARIC
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IRGRERFEMFRELNEALEL
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S38824

A;Cross-references: GB:M13874; NTD:g200202; R;Han, K.A.; Kulesz-Martin, M.F.
Nucleic Acids Res. 20, 1979-1981, 1992
A;Title: Alternatively spliced p53 RNA in transcrete number: S35478; MUID:92253421; FA;Accession: S35478 cellular tumor antigen p53, minor splice form - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change A; Molecule type: mRNA A; Residues: 1-381 < ARA> A; Reference number: S38822; A; Accession: S38824 C;Accession: S38824; S35478
R;Aral, N.; Nomura, D.; Yokota, K.;
Mol. Cell. Biol. 6, 3222-3239, 1986
A;Title: Immunologically distinct p5 ced p53 RNA in transformed and MUID:92253421; PMID:1579500 stinct p53 molecules MUID:87064640; PMID: Wolf, . : cules generated PMID:3023970 PIDN: AAA39883.1; Brill, [F] . bу normal cells of different PID:g200203 alternative splicing 23-Jul-1999 0.;

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A;Status: nucleic acid sequence not shown; A;Molecule type: mRNA

translation

not shown

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A; Residues: 1-381 <hAN>
A; Cross-references: EMBL:M13874; NID:9200202; PIDN:AAA39883.1; PID:9200203
A; Cross-references: EMBL:M13874; NID:9200202; PIDN:AAA39883.1; PID:9200203
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
C; Comment: This sequence, produced by alternative splicing of the tenth intron, lacks the south nown.
C; Superfamily: cellular tumor antigen p53
C; Reyvords: alternative splicing; phosphoprotein; zinc
F; 1-44/Domain: transcription activation #status predicted <TRA>
F; 1-26/Region: conserved region I
F; 99-289/Domain: DNA-binding core #status predicted <DBC>
F; 108-121/Region: Conserved region II
F; 160-192/Region: conserved region II
F; 161-192/Region: conserved region IV
F; 231-252/Region: conserved region IV
F; 231-252/Region: conserved region V
F; 313-319/Region: nuclear location signal
F; 319-319/Region: nuclear location signal
F; 319-357/Region: tetramer association
F; 7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F; 312/Binding site: phosphate (Ser) (covalent) #status predicted
F; 312/Binding site: phosphate (Ser) (covalent) by cdc2 kinase) #status predicted
                                                                                                                              tumor suppressor protein p53 - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 C;Accession: JC6176 R;Lee, H.; Larner, J.M.; Hamlin, J.L.
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A; Reference number: JC6176;
A; Contents: liver
A; Accession: JC6176
A; Molecule type: mRNA
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                                                               A; Title: Cloning and characterization of Chinese hamster A; Reference number: JC6176; MUID:97183659; PMID:9031625
                                                                                                       R; Lee, H.; Larner, J.M.; Hamlin, J.L.
Gene 184, 177-183, 1997
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;319-357/Region: tetramer association
;319-357/Region: tetramer association
;719-112.18.23.37/Bhinding site: phosphate (Ser) (covalent) #status predicted
;173,176,235,239/Binding site: zinc (Cys. His. Cys. Cys) #status predicted
;173,176,035,239/Binding site: covalent) (by cdc2 kinase) #status predicted
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A; Gene: p53
C; Superfamil
C; Keywords:
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A;Title: cDNA cloning and immunological characterization A;Reference number: JC6193; MUID:97208869; PMID:9055811
A;Accession: JC6193
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A;Residues: 1-393 <LEE>
A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230 C;Comment: This protein is a multimer, it plays the central role in a compliption, and recombination by protein/protein interactions.
C;Genetics:
                       δ.
                                                            В
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                                                                                                                                                                                           C; Superfamily: cellular tumor antigen
C; Keywords: tumor
                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-391 <LEA>
                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor suppressor
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                                                                                                                                                           Query Match
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                                                                                            11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
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157; Conserv
                                                                                                                                            Similarity
                            QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL-SPSPA----
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----VANWLNEDPEEGLRVPA---
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Pred. No. 5.2e-41;
51; Mismatches 116;
                                                                                                                           Score 699.5; DB 2;
Pred. No. 9.7e-41;
9; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53
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-APAPEA-PAPAAPALAAPAPATSWP
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RESULT 14
T19361

rotein C17G1.4 - Caenorhabditis elegans
hypothetical protein C17G1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.
C;Accession: T19361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
146226
cellular tumor antigen p53 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-Fe
C;Accession: I46226
                                       A;Residues: 1-925 <WIL>
A;Cross references: EMBL:278415;
A;Experimental source: clone C17GC;Genetics:
                                                                                                               submitted to the EMBL Data A; Reference number: Z19114 A; Accession: T19361
  A; Map position: 3
A; Introns: 40/3;
                                                                                       A; Molecule type: DNA
                                                                                                  A; Status: preliminary; translated
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C; Superfamily:
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A;Title: The canine p53 gene is subject to somatic mutations in A;Reference number: I46226; MUID:95150524; PMID:7847847
A;Accession: I46226
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A;Molecule type: DNA
A;Residues: 1-77 <DEV>
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                          CESP:C17G1.4
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   98/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:L27630;
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 295/1; 443/3;
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                                                                                                                                     Library, August
                                                     C17G1
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                                                               PIDN:CAB01670.1;
                                                                                                    from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                Score 259.5; DB 2;
Pred. No. 2.2e-11;
5; Mismatches 14;
 590/3; 619/3; 691/1;
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                                                               GSPDB:GN00028;
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A; Decube type: DNA
A; Molecule type: DNA
A; Residues: 1-1621 <JOH>
A; Cross-references: EMBL: AF003386; NID: g2088833; PID: g2088843; PIDN: AAB54259.1;
A; Cross-references: Strain Bristol N2; clone F59E12
                                                                                                                                                                                                                                                                                                                                                            R;Johnson, D. submitted to the EMBL Data Library, May 1997 a. Description: The sequence of C. elegans co
                                                                                                                                                                                                                                                                                                                      A; Description: The sequence
A; Reference number: Z18318
A; Accession: T15264
                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F59E12.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te;C;Accession: T15264
                                                                                                                            A; Map position: A: Introns: 30/3;
                                                                                                                                                                            A; Gene: CESP:F59E12.9
                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 23.3
Matches 127; Conservative
                                           Local Similarity
les 111; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNEGQIAPPSHLIRVEG-NSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPIQIK----VMTPP----PQGAVIR-----AMPVYKKAEHV---TEVVKRCPNHELSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYQIEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLNSNNAAGLPPLSLRSQGPDGSQNNDFPGIPSTSS--SNQAHALCAGC-HHFIMPGSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPQKKKHEDGVPEPPTADTPFTTVTHYELPAAMTFLRDTLHVGPNDKVHPQVEKHYFSRK
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                                             Conservative
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                                                                                                                            200/2; 299/2; 327/2; 369/3; 589/3; 860/1; 986/1; 1278/1; 1547/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PPLSM----PSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTT
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-FLSPEVFQHIWDFLEQPICSVQPIDL---
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                                                               Score 144.5; D
Pred. No. 0.14;
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                                           Gaps
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Qy	Фр	Од	Qу	Оy	Оy	Оy	Оy	Ф	дb
482 1378	422 1333	365 1280	314 1224	25 4 1197	195 1143	135 1088	80 1028	46 968	920
PTQALPPDLSMPSTSHCTPPPPPYPTD 507	NSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLS 481	PVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYG 421	KADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYL 364 : ::	PQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR 313	AEHVTEVVKRCPNHELSREFNEGQIAP-PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP 253 :	PHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKK 194	SMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSP-AIPSNTDYPG 134	ATNKIEISMDCIR	

Search completed: August 7, 2003, 09:53:19 Job time: 23.2089 secs

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Run

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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        SwissProt_41:*
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        GenCore version (c) 1993 - 2003
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P53_ONCAY
P53_BARBU
P53_BRARE
P53_ICTPU
P53_YENLA
P53_PICAY
P53_PICAY
P53_PICAY
P53_CAYLA
P53_CAYLA
P53_CAVPO
P53_RAT
P53_CAVPO
P53_HUMAN
P53_MACGA
P53_MOUSE
P53_MOUSE
P53_MOUSE
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P53_CAYLA
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Compugen Ltd.
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Q9xsk8 cercopithec
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5 oncornynchu
barbus barb
4 brachydanio
4 brachydanio
5 ictalurus p
3 xenopus lae
9 tetraodon m
2 sus scrofa
5 felis silve
0 gallus gall
7 canis famil
10 oryzias lat
8 bos taurus
6 marmota mon
1 rattus norv
6 cavia porce
1 tupaia glis
4 ovia aries
4 ovia aries
6 mesocricetu
6 platichthys
7 homo sapien
0 mus musculu
3 macaca fasc
1 cercopithe
6 xiphophorus
5 xiphophorus
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6 xiptophorus
7 xiphophorus
7 xiphophorus
8 xiphophorus
9 cricetulus
10 cercopitius
11 cercopitius
12 equus cabal
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Result No.

Minimum Maximum

DB Bd

Searched:

Database :

444440 335 4444 444 443 443 443
143.5 141.5 138 134.5 130.5 130.5 129.5 129.5 129.1 12
4444 4444 444 444 444 444 444 444 444
5147 1081 1520 1386 1544 628 766 589 964 766 921 628
PCLO_HUMAN GALY_YEAST ABL_DROME ZAP3_MOUSE TUSP_HUMAN Y10K_TYMVC TLE4_MOUSE SPY_DROME Y0KA_SCHPO TLE4_HUMAN T2D3_DROME Y70K_TYMV
Q9y6v0 P19659 P00522 Q9r017 Q9rr14 P28478 Q62441 Q62441 Q644783 Q644783 Q74522 Q04727 P47825 P10357
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ALIGNMENTS

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SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA). TISSUE-Breast cancer, Hepatoma, Lymphocytes, and Skin; MEDLINE-99310938; PubMed-10381648; De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G., Costanzo A., Levrero M., Knight R.A.; "Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";	ESQUENCE FROM N.A. ISSUE-Neuroblaston EDLINE-99021697; Cos e Laurenzi V., Cos nnicchiarico-Petru Two new p73 splice ranscriptional act Exp. Med. 188:17 5]	SEQUENCE FROM N.A. (ISOFORM ALPHA). MEDLINE=98389621; PubMed=9721206; Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Jenkins R., Smith D.I., Liu W.; "Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions."; Genomics 51:359-363(1998).	SEQUENCE FROM N.A. (ISOFORM ALPHA). SEQUENCE FROM N.A. (ISOFORM ALPHA). MEDILINE-99289209; PubMed-10362363; YOShikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K., Harris C.C.; "Mutational analysis of p73 and p53 in human cancer cell lines."; Oncogene 18:3415-3421(1999).	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA). SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA). TISSUE-Colon; MEDLINE-97433090; PubMed-9288759; MEDHINE-97433090; PubMed-9288759; MEDHINE-97433090; PubMed-9288759; MINTY A., Bonnet H., Yang A., Creancier L., Biscan JC., Valent A., Minty A., Chalon P., Lelias JM., Dumont X., Ferrara P., McKeon F., Caput D.; "Monoallelically expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers."; Cell 90:809-819(1997).	RESULT 1 P73_HUMAN STANDARD; PRT; 636 AA. C 015350; 015351; Q9NTK8; T 16-OCT-2001 (Rel. 40, Created) DT 16-OCT-2001 (Rel. 40, Last sequence update) T 15-SEP-2003 (Rel. 42, Last annotation update) E Tumor protein p73 (p53-like transcription factor) (p53-related DE protein). A TP73 OR P73. Homo sapiens (Human). C Mammalia; Eutheria; Craniata; Vertebrata; Euteleostomi; C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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"Natl.
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Kaelin W.G. Jr.;
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Kharbanda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to DNA damage.";
Nature 399:814-817(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99318135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                 TISSUE SPECIFICITY: BRAIN, KIDNEY, PI
SPLEEN, SKELETAL MUSCLE, PROSTATE, TH
INDUCTION: NOT INDUCED BY DNA DAMAGE.
                               DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.

DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
                                                                                                                                                                                                                                                                     Name-Zeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. 18.4438-4445(1999).

FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE. WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                   NEUROBLASTOMA AND
                                                                                                                                                                                                                                                                                                                                                                  Name=Epsilon;
                                                                                                                                                                                                                                                                                                                                                                                                        Name=Delta;
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INE-99318135; PubMed=10391251;
Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,

banda S., Weichselbaum R., Kufe D.;
is regulated by tyrosine kinase c-Abl in the apoptotic response
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Note=The splicing
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IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN COLICODENDROGLIOMA.

GS TO THE BET TO AND TO BE FREQUENTLY MUTATED IN COLICODENDROGLIOMA.
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GO; GO:0003700; F:transcription factor activity; TAS.
GO; GO:00008530; P:induction of apoptosis by DNA damage;
GO; GO:00006298; P:mismatch repair; TAS.
InterPro; IPR0012117; P53.
InterPro; IPR001260; SAM.
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TRANSFAC; T04931;
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the European Bioinformatics Institute. There a
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3D-structure.
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DCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
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                                                                                                                                                                                                                                                                        POLY-GLN.
                                                                                                                                                                                                                                                                                                                   MEDIATES
                                                                                                                                                                                                                                                                                                                                          ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                             TRANSACTIVATION
                                                                                                                                             GNTRCRHWVLCGDRGLSRPVLQGPSG
                                                                                                                                                                                                                                                                                                                   OLIGOMERIZATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ormatics and the EMBL outst
There are no restrictions
ong as its content is in
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ormatics and the EMBL outstation -
                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                          (BY
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CENTRAL DNA

THAT BINDS

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Best Local (
                                                                                                                                                                                                                                                                                                                                CERAE
                                                                                                                                                                                                        O9XSK8: Q9TSQ9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein p73 (p53-like transcription factor) (p53-related
                                                                                                          Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                          protein).
TP73 OR P73.
                                                                                                Cercopithecinae;
                                                                                                                                                                                                                                                                                                            P73_CERAE
                      TISSUE-Kidney;
                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 366; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGTH---MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSTVSFLARLGCSSCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVLGRRCFEARICACPGRDRKADEDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEDIMSPAPVIPSNIDYPGPHHFEVTEQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSQSTQTNEELSPE---VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI----EIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATISIGGSGELQRQRVMEAVHFRVRHTITIPNRGGPGGGPDEWADFGFDLPDCKARKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASTVSV-GSSETRGERVIDAVRFTLRQTISFPPR-----DEWNDFNFDMDARRNKQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDLKQGHDYSTAQQLLRS-SN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPSHLQ-PPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGPG----M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVLGRRSFEGRICACPGRDRKADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDVFHLEGMTTS - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                               639
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                Cercopithecus.
                                        (ISOFORMS ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNEVVGGTDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.6e-113;
4; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1790;
Pred. No. 2
                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                          637
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                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   625
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                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Swed http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE DAN DAMAGE.
-- FUNCTION: PROMICED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y11419; CAA72224.1;
EMBL; Y11419; CAA72225.1;
HSSP; O15350; 1COK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOId-Q9XSK8-2; Sequence-VSP 006537;
DOMAIN: POSSESS AN ACIDIC TRANSACTIVATION DOMAIN, A CE
BINDING DOMAIN AND A C-TERMINAL OLICOMERIZATION DOMAIN
TO THE ABL TYROSINE KINASE SH3 DOMAIN.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: THE C-TERMINAL OLIGOMERIZATION D
TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA
AND WITH P53, WHEREAS ISOFORM ALPHA DOES
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                            163
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                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                    AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDG
                                                                                        MDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                                                                                                                                                                                                                                            MAQSTTT----SPDGGTTFEHLWSSLEP-----DSTYFDLPQSSRGNNEVVGGTDSS
                                                                                                                                                                                                                                                                                                                                                                 MSQSTQTNEFLSPE----VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI----EIS
                                                                                                                                                                                                                                                MDVFHLEGMTTS-----VMAQFNLLSSTMDQMSSRAASASPYTPEHAA-SVPTHSPYAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     637
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABLE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY WHEREAS ISOFORM ALPHA DOES NOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69630
                                                                                                                                                                                                                                                                                                                                                                                                                     54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1769.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_006537.
7CB200B919C9C70A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     ed. No. 6.2e-112;
Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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Indels Length

Gaps

17

5

48

173

102

233 222

637; 59;

Indels Length 396;

55;

Gaps

10;

188 147

266 308 206 248 128

39

87

(ACIDIC) Activator;

(POTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P25035;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
7-11.1ar fumor antigen p53 (Tumor suppressor
                                                                             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92210006; PubMed=1339362; de Fromentel C.C., Padkel F., Chapus A., "Ratanbow trout p53: cDNA cloning and bioc Gene 112:241-245(1992).

-I- FUNCTION: Acts as a tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Actinopterygii, Reopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
                        EMBL; M75145; AAA49605.1; PIR; JH0631; JH0631.
                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P53_ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
                                                                                                                                                                                                                                     BAX and FAS antigen expression, or by repexpression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||:||| :|| ::: :::|| :||||||:| ||:|: | :| |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : | |:: : : : | |:: : : | |:: : : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : | |:: : : : | |:: : : : | |:: : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : : | |:: : : | |:: : : | |:: : : : | |:: : : : | |:: : : | |:: : : : | |:: : : | |:: : | |:: : | |:: : : | |:: : : | |:: : | |:: : | |:: : : | |:: : | |:: : | |:: : : | |:: : : | |:: : : | |:: : | |:: : | |:: : : | |:: : : | |:: : | |:: : | |:: : : | |:: : | |:: : | |:: : | |: : : | |:: : | |:: : | |:: : | |:: : | |:: : | |: : | |:: : | |: : | |:: : | |: : | |: : | |: : | |: : | |: : | |: : | |: : | |:
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biochemical
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P53_BARBU
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Best Local
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DOMAIN
DOMAIN
P53_BAR
Q9W678;
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MOD_RES
                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor)
                                                                                                                                                                                                                    Actinopterygii; Neopterygii; Cyprinidae; Barbus. NCBI_TaxID=40830;
                                                                                                                                                                                                                                                                                                  Barbus barbus (Barbel).
                                                                                                                                                                                                                                                                                                                       TP53 OR P53
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                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00386; P53SUPPRESSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSDYPGALGFQLRFLQSSTAKSVTCTYSPDLNKLFCQLAKTCPVQIVVDHPPPPPGAVVRA
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356
392
318
                                                                                                                                                                                                                                                                            Chordata;
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Pred. No. 4.8e-
61; Mismatches
                                                                                                                                                                                                                                                         ; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tion; Apoptosis.
TRANSCRIPTION ACTIVATION
BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTEN PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8422250765545A1C CRC64;
                                                                                                                                                                                                                                                                                                                                         suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                847.5; DB 1;
No. 4.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                         369
                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KMNLNLVAVQPPETE----SWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                BRARE
                                  P53_BRARE STANDARD; PRT; 373 AA. P79734; Q90440; P79734; Q90440; Q1-NOV-1997 (Rel. 35, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor TP53 OR DRP53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-oncogene; DNA-binding; Transcription regulation; Activator;

Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 66 256 BY SIMILARITY.

DOMAIN 298 329 OLIGOMERIZATION.

DOMAIN 342 365 BASIC (REPRESSION OF DNA-BINDING).

DOMAIN 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

MOD_RES 368 368 PHOSPHORYLATION (BY SIMILARITY).

SEQUENCE 369 AA; 41233 MW; OBEZCF2CEA74C304 CRC64;
             Brachydanio rerio (Zebrafish) (Danio Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF071570; AAD34212.1; -. HSSP; P04637; 1TUP.
 Actinopterygii; Neopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptam; PF00870; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apoptosis
BAX and F/
                                                                                                                                                                                                                                                                                                                        196
                                                                                                                                                                                                                                    374
                                                                                                                                                                                                                                                                 256
                                                                                                                                                                                                                                                                                              323
                                                                                                                                                                                                                                                                                                                                                                                   138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                     263
                                                                                                                                                                                                                                                                                                                                                                                                             203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                     PQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMVVNVAPPQGSVIRATAIYKKSEHVAEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTEDALSPSPAIPSNTDYPGPHSEDVSF
                                                                                                                                                                                                                                 MLLKIKESLELMOYLPOHTIETYROO
                                                                                                                                                                                                                                                              DQ---ETKTLDKIPSANKRSLTKDSTSSVPRPEGSKKAKLSGSSDEEIYTLQVRGKERYE
                                                                                                                                                                                                                                                                                        QQVSDSTKNGD----GTKRPF-RQNTHGIQMTSIKKRR----SPDDELLYLPVRGRETYE 373
                                                                                                                                                                                                        MLKKINDSLELSDVVPPSEMDRYRQK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELINDEYLPSSFDPNIFDNVLTEQPQPSTSP-----PTASVPVATDYPGEHGFKLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is induction seems to be mediated either by stimulation FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.1%;
51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 819.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                        suppressor p53).
                                                                                                                                                                                                                                   399
             rerio).
ta; Vertebrata;
Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .3e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
             Euteleostomi;
Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                              312
                                                                                                                                                                                                                                                                                                                        255
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                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S., Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.; "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence expression during embryogenesis."; Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
                                                                                                                                                                                                                                                                                                                                                          Anti-oncogene; DNA-binding; Transcription regulation; Activator; nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 70 260 BY SIMILARITY.

DOMAIN 301 332 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U60804; AAB40617.1; -
EMBL; U46693; AAA97408.1; -
HSSP; P04637; lTUP.
ZFIN; ZDB-GENE-990415-270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyprinidae; Danio
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002117; Pfam; PF00870; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Winge P.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 140-212 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97344388; PubMed=9200835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (Br Similarity).

SUBCULTULAR LOCATION: Nuclear.

SYMILARITY: BELONGS TO THE P53 FAMILY.
                                       169
                                                                                                   292
                                                                                                                                                                                                  112 QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
                                                                                                                                                                                                                                                Similarity
    DGQVLGRRCFEARICACPGRDRKADEDSIRK-QQVSDSTKNGDGTKRPFRQNTHGIQM--
                                      QPST----LPPTSTVPETSDYPGDHGFRLRFPQSGTAKSVTCTYSPDLNKLFCQLAKTCP
                                                                       SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR
                                                                                                                                                                                                                                                                                             70
301
345
280
272
373 AA;
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                               260
332
366
296
372
                                                                                                                                                                                                                                                                                                41899 MW;
                                                                                                                                                                                                                                                23.7%;
53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . . .
                                                                                                                                                                                                                                 42; Mismatches
                                                                                                                                                                                                                                                Score 805.5; DB Pred. No. 3e-47;
                                                                                                                                                                                                                                                                                             NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
AC7AB724FA6B61FF CRC64;
                                                                                                                                                                                                                                                                                                                                            BASIC (REPRESSION OF
                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                            DNA-BINDING)
                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                     291
                                      228
                                                                                                   168
                                                                                                                                   231
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EGQLLGRRSFEVRVCACPGRDRKTEESNFKKDQETKTMAKTTTGTKRSLVKESSSATLRP

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349 289

399

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RESULT 6
P53_UCM
P53_U
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Best Local
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093379;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor FP53 OR P53.
                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Luft J.C., Bengten E., Clem L.W., Miller N.W., "Identification and characterization of the tunchannel catfish (Ictalurus punctatus)."
Comp. Biochem. Physiol. 120B:675-682(1998).
                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00348; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF074967; AAC26824.1; HSSP; P04637; ITUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=99071979; PubMed=9854815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinopterygii; Neopterygii; Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                   108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P04637;
     56
                                                                                                                                     Similarity
SDMLQPQSS--SSPPTSTVPVTSDVPGLLNFTLHFQESSGTKSVTCTYSPDLNKLFCQLA
                                                 SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGSKKAKGSSSDEEIFTLOVRGRERYEILKKLNDSLELSDVVPASDAEKYROK 341
                                                                                                                                                                                                             303
347
286
375
376
                                                                                                          Conservative
                                                                                                                                                                                                                  A,
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD
                                                                                                                                                                                                                                                                                                                                                                Phosphorylation; Apoptosis.
36 TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Channel catfish).
Chordata; Craniata;
                                                                                                                                                                                                                  41989
                                                                                                                                   23.3%;
                                                                                                                                                                                                                  ¥
                                                                                                     Score 795; DE
Pred. No. 1.5e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Teleostei;
                                                                                                                                                                                                             NUCLEAR LOCALIZATION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
1B89CD98DB3289F2 CRC64;
                                                                                                                                                                                                                                                                                                                  BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the tumor
                                                                                                                           DB 1;
.5e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ostariophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson
                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suppressor p53
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.R.;
                                                                                                                                                                                                                                                                                                                                                                        (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              induces
                                                                                                     Gaps
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113
                                                   167
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P53_XENLA
ID P53_X
ID
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                   EMBL; M36962; L
EMBL; X05191; (
EMBL; X77546; (
EMBL; S68353; A
PIR; A29376; A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In Xenopus laevis embryos.";
In Xenopus laevis embryos.";
Oncogene 9:109-120(1994).

-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53_XENLA
P07193;
01-APR-1988
                                                                                                                                                                                        or send
                                                                                                                                                                                                                                            modified
                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinfo
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=94134403; PubMed=8302570;
Hoever M., Clement J.H., Wedlich D., Montena
"Overexpression of wild-type p53 interferes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soussi T., de Fromentel C.C., Mechali M., May P., Kress M.; "Cloning and characterization of a cDNA from Xenopus laevis coding for a protein homologous to human and murine p53."; Oncogene 1:71-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=88143684; PubMed=2830576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cellular tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1988
28-FEB-2003
                                                                                                                                                                                                              entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                             expression (By similarity).

SUBUNIT: Binds DNA as a homotetramer (
SUBCELLULAR LOCATION: Nuclear:

TISSUE SPECIFICITY: Ubiquitous.

SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration -een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114
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                                                                                                                                                                                        an
                                                                                                                                                                                                                                      and this statement is not removed
                                                                                                                                                                                                                                                                  non-profit institutions as long
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. 07, Last
. 41, Last
                                                                                                                                                                                     license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniáta; Vertebrata; Euteleostomi; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                   Usage
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A29376.

; AAA49923.1; ; CAA28821.1; ; CAA54672.1; ; AAC60746.1;

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InterPro; IPR002117; P53.

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Best Local S
Matches 171
                                                                                                                                                                                                                                                                        TETMU
                                                                                                                                                                    P53_TETMU STANDARD; PRT; 367 AA. 09W679; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor | TF53 OR P53.
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DOMAIN
DOMAIN
DOMAIN
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Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
"Evolutionary conservancy of p53 gene sequences in fish.";
Submitted (JUN1-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Acts as a tumor suppressor in many tumor type
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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                                                    TISSUE=Ovary;
                                                                                           NCBI_TaxID=94908;
                                                                                                                                                            Tetraodon miurus (Congo puffer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPPPRGSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYM
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363
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

T -> S (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).

CELF3E58F020D74D CRC64;
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Pred. No. 2.7
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tumor types;
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DOMAIN 1 47 TRANSCRIPTION ACTIVATION DNA_BIND 86 273 BY SIMILARITY.

DOMAIN 308 337 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF071571; AAD34213.1; -. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002117; P53.
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European Bioinformatics Institute. T
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression (By similarity).
SUBUNIT: Binds DNA as a homot.
SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation capacity and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE P53 FAMILY.
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LQIRGRKRYEMLKKINDGLDLLENKPK
                          LPVRGRETYEMLLKIKESLELMQYLPQ 390
                                                                                                      GRDRKTEETNSTKMQ------NDAKDAKKRKSVPTPDSTTIKKSKTASSAEEDNNEVYT
                                                                                                                                GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS------PDDELLY
                                                                                                                                                                                                    PYEPPQLGSEFTTILLSFMCNSSCMGGMNRRPILTILTLETQEGIVLGRRCFEVRVCACP
                                                                                                                                                                                                                              PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP
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Pred. No. 2.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY).; ACC10EEE2F5F9CFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Bioinformatics and the EMBL outstation
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RESULT 9 P53_PIG ID P53_PIG

STANDARD;

PRT;

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Q9TUB2; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor

p53).

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                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P04637;
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"Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-99422034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002117; p53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant porcine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: p53 is found in increased amounts of transformed cells. p53 is frequently mut in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression.
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLURAR LOCATION: Nuclear.
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                                            QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNT
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                                                                                        LSQETFSDLWKLLPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P53;
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45 TRANSCRIPTION ACTIVATION
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the porcine p53 cDNA,
                                                                                                                                                                                                                                                                        Œ;
                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation;
                                                                                                                                                                           Score 771; DB
Pred. No. 6.6e
i8; Mismatches
                                                                                                                                                                                                                                                                                                                    SIMILARITY)
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                                                                                                                                                                                                                                                                      A4C3D88E8DF55162
                                                                                                                                                                                                                     771;
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6.6e-45;
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-PAATAPAPAAPAPATSWPL--SSFVPSQK 93
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Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and chromosomal mapping of feline p53 tumor suppressor gene.";
J. Vet. Med. Sci. 55:801-805(1993).
I. FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P53_FELCA
P41685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 34-354 FROM N.A.
MEDLINE-94114699; PubMed-8286534;
Okuda M., Umeda A., Watsumoto Y., Momoi Y., Watari
O'Brien S.J., Tsujimoto H., Hasegawa A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TP53 OR TKF33.
Felis silvestris catus (Cat).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Fissipedia; Felidae;
                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okuda M., Umeda A., Sakai T., Ohashi T., Momo Watarī T., Goltsuka R., Tsujimoto H., Hasegav "Cloning of feline p53 tumor-suppressor gene hematopoletic tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Lymph node;
MEDLINE-94333960; PubMed-8056458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Int. J. Cancer 58:602-607(1994).
                                                                                                                                                                                                                                                                                                       expression.
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                   in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                             DISEASE: p53 is found in incr
of transformed cells. p53 is
                                                                                                                                                                                                                                                                                                                                                                                                                                     circumstances and cell type. Involved in cell cycle regulation a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases appoptosis induction seems to be mediated either by stimulation of the activated genes is an inhibitor of cyclin-dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                          BAX and FAS antigen
                                                                                                                  SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330
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Tsujimoto H., Hasegawa A.;
tumor-suppressor gene and i
                                                                                                                                                                                                                                                                                                                                                                                                             expression,
                                                                                                                                                                                                                                                                                           increased amounts
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                                                                                                                                                                                                                                                                                                                                                                                                          mediated either by stimulation or by repression of Bcl-2
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                                                                                                                     a collaboration
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p53 nuclear

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P53_CHIT 11
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D7 01_MA
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Best Local :
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                                                                                                                                                                                  01-MAR 1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA_BIND
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EMBL; D16460; BAA03977.1;
HSSP; P04637; 1DLG.
InterPro; IPRO02117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                               Gallus gallus (Chicken)
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    STRAIN-SPAFAS;
                     SEQUENCE FROM N.A
                                                               NCBI_TaxID=9031;
                                                                                                      Archosauria;
                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                      Chordata; Craniata; Vertebrata; Neognathae; Galliformes; Phasian:
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PHOSPHORYLATION (BY SIMILARITY).
K -> R (IN REF. 2).
D08B43BA1BC8EB78 CRC64;
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                                                                                                      Phasianidae; Phasianinae;
                                                                                                                                                                                      p53).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
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MOD_RES
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DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 87 278 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13057; CAA31456.1; PIR; S02193; S02193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 16:11383-11383(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oncoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P04637; 1TUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89083584; PubMed=3060861;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis induction seems to be mediated either by st. BAX and FAS antigen expression, or by repression of B expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
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GRETYEMLLKIKESLELMQ 386
                                                            GRDRKADEDSIRKQQVSDSTKNGDG--TKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVR
                                                                                                                                               PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                  TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
                                                                                                                                                                                                                                  PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEPTEVFMDLWSMLPY---SMQQL-----PLPEDHSNWQELS----PLEPSDPPPPPP
                                         GRDRKIEEENFRK-----RGGAGGVAKRAMSPPTEAPEPPK-KRVLNPDNEIFYLQVR
                                                                                                                         PYEPPEVGSDCTTVLYNFMCNSSCMGGMNRRPILTILTLEGPGGQLLGRRCFEVRVCACP
                                                                                                                                                                                                            AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
                                                                                                                                                                                                                                                                                                                                                                                                                      PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                               EDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKVYCRLAKPCPVQVRVGVAPPPGSSLRAV
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kraegel S.A., Pazzi K.A., Madewell I "Sequence analysis of canine p53 in Cancer Lett. 92:181-186(1995).
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28-FEB-2003 (Rel. 41, Last
Cellular tumor antigen p53
                                          Pfam; PF00870; P53; 1.
PRINTS; PP00777
                                                                                                     EMBL; AB020761; BAA78379.:
EMBL; S77819; AAB42022.1;
HSSP; P04637; lOLG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora; 
MCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q29537; Q9TV78;
01-NOV-1997 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watari T., Hasagawa
"Aberrations of p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Setoguchi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Leukocyte;
MEDLINE=98178696;
  PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
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                                                                                                                                                                                                               send
                                                                                                                                                                                                                                                                                                                                                                                   in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: p53 is found in increased amount of transformed cells. p53 is frequently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Acts as a tumor suppressor in many
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                                                                                                                                               AF060514; AAC16909.1; AR020761; BAA78379.1;
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               PR00386; P53SUPPRESSR.
PD002681; P53; 1.
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  PS00348;
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(DEC-1998) to
                                                                                                                                                                                                               email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAS antigen expression,
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Tsujimoto
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annotation update)
(Tumor suppressor
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H.;
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Nuclear protein;
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                                                                                                                                                                                                                                                                        LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSD-PMW
                                                                                                                                                                                      TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
ERYEMFRNLNEALELKDAQSGKEPGGSRAHSSHLKAKKGQSTSRHKKLMFKREGLDS
                                                                                    ETYEMLLKIKESLELMQYLP-
                                           GRDRRTEEENFHKKGEPCPEPPPGSTKRALPPST---SSSPPQKKKPLDGEYFTLQIRGR
                                                                GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                          PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                AIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRNTFRHSVVV
                                                                                                                                                   PYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                         KTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLWVSSPPPPNTCVRAM
                                                                                                                                                                                                                                        PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
                                                                                                                                                                                                                                                              LSQETFSELWNLLPE-----NNVLSSELCPAVDELLLPESVVNWLDEDSDDAPRM
                                                                                                                                                                                                                                                                                                                                                     381
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                                                                                                                                                                                                                                                                                                                                                                                                                  313
356
299
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                    378
42486
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4
                                                                                                                                                                                                                                                                                                                    22.3%;
                                                                                                                                                                                                                                                                                                                                                     ₹;
                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                       Score 758.5;
Pred. No. 4.5e
63; Mismatches
                                                                                                                                                                                                                                                                                                                                                              F
                                                                                                                                                                                                                                                                                                                                                              MEES -> MQEP (IN L -> P (IN REF. )
                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                     761A718FDC93DA59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis
                     -QHT---IETYRQQQQQQHQHLLQKQTSIQS
                                                                                                                                                                                                                                                                                                                    4.5e-44;
                                                                                                                                                                                                                    ATSAPTAPGP--APSWPL----SSSVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation;
                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                           129;
                                                                                                                                                                                                                                                                                                                             1,
                                                                                                                                                                                                                                                                                                                                                                        REF.
                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         PRPK)
                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-BINDING)
SIGNAL (POTE
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                        2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activator;
                                                                                                                                                                                                                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                381;
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                         61;
                                                                                                                                                                                                                                                                                                        Gaps
                     416
 380
                                                                 369
                                                                                                                                                                        147
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                                                                                                          309
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RESULT 13
P53_OF3_C
AC P798_C
AC ACAN
OC ACAN
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OC ACAN
OC ACAN
C
ACAN
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Futeleos Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzins NCBI_TaxID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last ann
28-FEB-2003 (Rel. 41, Last ann
Cellular tumor antigen p53 (Tu
                                                                                                                       exposed
                                                                                                                                                    Krause M.K., Rhodes L.D., van Beneden R.J.; "Cloning of the p53 tumor suppressor gene f (Oryzias latipes) and evaluation of mutatio
                                                                                                                                                                                                                                                                               MEDLINE=97305153; PubMed=9161419;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P53_ORYLA (
P79820; Q9PSU7;
01-NOV-1997 (Re:
        SEQUENCE
                                                                                  Gene
                                                                              189:101-106(1997).
                                                                                                                           fish.";
        FROM
                                                                                                                                                                                                                                                                                                                                                         N.A.
    Ν.Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD; ; Q9PSU8;
    AND
        VARIANT THR-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
annotation update)
(Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                mutational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352
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                                                                                                                                                                                             from
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                                                                                                                                                        hotspots
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Best Local (
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Himedaka;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression (By similarity).
SUBUNIT: Binds DNA as a homote
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Acts as a tumor suppressor in many tumor
                             207
                                                                                   152
                                                                                                             196
                                                                                                                                                                     136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF003949; AAD01195.1; -AF003950; AAD01196.1; -P04637; 1YCS
                                                                                                                                                                                                                                                                                                             163;
                                                                                                                                        92
                                                                                                                                                                                               56
                                                                                                                                                                                                                           76
                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
                                          VGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKA
DEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS-----PDDELLYLPVRG
                                                                                               EHVTEVVKRCPNHELSREFNEGGIAPPSHLIRVEGNSHAQVVEDPITGRQSVLVPYEPPQ
                                                                                                                                        YELELRFOKSGTAKSYTSTYSETLNKLYCOLAKTSPIEVRVSKEPPKGAILRATAYYKKT
                                                                                                                                                                 HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKA
                                                                                                                                                                                                 ---GTFDDKI---
                                                                                                                                                                                                                       GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGP
                                                                                                                                                                                                                                                    FQELWETVSYP--PLETLSLPTVNEPTGSW-----VATGDMFLLDQDLS---
                                                                                                                                                                                                                                                                                FQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQYTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requires a license agreement (See http://www.isb-sib.ch/announce/
                          PGSEMTTILLSYMCNSSCMGGMNRRPILTILTLET-EGLVLGRRCFEVRICACPGRDRKT
                                                                                   EHVADVVRRCPHHQ
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC60146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                           273
331
350
350
295
351
91
91
22
39753 MW;
                                                                                                                                                                                                                                                                                                                       21.9%;
                                                                                  ----NEDSVEHRSHLIRVEGSQLAQYFEDPYTKRQSVTVPYEPPQ
                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homotetramer (By
                                                                                                                                                                                                                                                                                                            Pred. No. 2.604; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY SIMIL S -> T.
MISSING (IN REF. 1).
196868A66351BFF5 CRC64;
                                                                                                                                                                                                                                                                                                                         Score 746.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                          BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSCRIPTION ACTIVATION (AC
                                                                                                                                                                                            ----FDIP----IEPVPTNEVNPPPTTVPVTTDYPGS
                                                                                                                                                                                                                                                                                                          i.6e-43;
ies 92;
                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-BINDING).
SIGNAL (POTENTIAL)...
                                                                                                                                                                                                                                                                                                                                      Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.P.H.;
                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      types;
                                                                                                                                                                                                                                                                                                            69;
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                                                                                                                                                                                                                                                                                                          Gaps
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368
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PS3_BULT
P53_BULT
P53_BULT
P79_BULT
P59_BULT
P59
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Q29628;
Q1-NOV-1997
Q1-NOV-1997
28-FEB-2003
                                                                                                                                      EMBL; X81704; CAA57348.1; -. EMBL; D49825; BAA08629.1; -. EMBL; U74486; AAB51214.1; -.
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishop R.R.P., Gobright E.E.I.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=Bovine; TISSUE=Liver; MEDLINE=95352829; PubMed=7626789;
                                                                             PIR; S51648; S51648.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=B.indicus; STRAIN=Boran;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dequiedt F., Kettmann R., Burny A., Willems L.; "Nucleotide sequence of the bovine P53 tumor-suppressor cDNA."; DNA Seq. 5:261-264(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
NCBI_TaxID=9913, 9915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida "Predominant p53 mutations in enzootic bovine leukemic ovet. Immunol. Immunopathol. 52:53-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-Bovine; STRAIN-Holstein; MEDLINE-96401400; PubMed-8807776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 13-386 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of transformed cells. point many types of cancer SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression.
SUBUNIT: Binds DNA as a h
SUBCELLULAR LOCATION: Nuc
DISEASE: p53 is found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     indicus (Zebu).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RERYEFLKKINDGLELLE
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(Rel. 35,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BELONGS TO THE P53 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruminantia; Pecora; Bovoidea;
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PRINTS; PR00386; InterPro;

P53SUPPRESSR.

PF00870;

IPR002117; P53.

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P53_MARP
P53_MARP
P53_MARP
ID P58
AC 03
DT 166
DT 166
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CC Ma
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Matches
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                                                                                                                                             "Partial characterization of the woodchuck tumor its interaction with woodchuck hepatitis virus X hepaticarcinogenesis.", Oncogene 15:327-336(1997).
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16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
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                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-97376996; PubMed-9233767;
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                                                      Marmota monax (Woodchuck)
                                                                                                                                                                                                                                                                                                                                                                                                                             Cellular tumor
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Local
FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPILTIITLEDSCGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGQSCPEPPPRSTKRAL
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TRANSON
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Rođentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
annotation update)
(Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 740; DB
Pred. No. 8.1e
57; Mismatches
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BASIC (REPRESSION
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                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata;
Sciurognathi; Sciurida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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No. 8.1e-43;
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                                                                                                                                                                                                                                                                                                                                                Sciuridae;
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                                                                                                                                                                                                                         Zhang
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antigen in
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SIGNAL (POTE)
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                                                                                                                                                                                                                                                                                                                                             Sciurinae;
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                                                                                                                                                                                                        p53,
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SEQUENCE
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DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00348; P53; 1. Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
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SIMILARITY: BELONGS TO THE P53 FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
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en the Swiss Institute of Bioinformatics
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transformed cells. p53 is
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                                                                                     VRVCACPGRDRRTEEENFRKR-----
                                                                                                 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNT----
                                                                                                                                                                                                                                     ---IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
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                   LQKQTSIQSPSS
                                          DGEYFTLKIRGRARFEMFQELNEALELKDAQAEKEPGESRPHPSYLKSKKGQSTSRHKKI
                                                               DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHT--
                                                                                                                                                                           GTRVRAMAIYKKSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGNLRAEYLDDRNT
                                                                                                                                                                                                                      SSSVPSQNTYPGVYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWVDSTPPP
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OLIGOMERIZATION.
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Pred. No. 1.1e-42;
0; Mismatches 121;
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E1DE5DB84BA40182 CRC64;
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SIGNAL (POTENTIAL).
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Result
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Q9h3d4 homo sapien
Q9ue10 homo sapien
Q9ue10 homo sapien
Q9yje3 rattus norv
Q9jjp6 rattus norv
Q9jjp6 rattus norv
Q9jb6 homo sapien
Q9plb4 homo sapien
Q9plb4 homo sapien
Q9plb6 homo sapien
Q9plb7 mus musculu
Q9yje2 rattus norv
Q9dec7 gallus gall
Q9plb7 homo sapien
Q9pld8 rattus norv
Q99jd8 rattus norv
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ALIGNMENTS

	EMBL: AF124534:	EMBT. AF124533	EMBL; AF124532;	•	•••	EMBL; AF124528;	DR EMBL; AF124539; AAG45	-i- SI	-!- SUBCELLULAR	RL Submitted (NOV-2002) to the	Strausberg	<pre>RC TISSUE=Lymph;</pre>	[3]	Submitted	Hagiwara K	RP SEQUENCE FROM N.A.	RL Mol. Cell 2:305-316(1998).	RT transactivating, deat	RT "p63, a p53 homolog at 3q27-29,	RA Andrews N.C., Caput I	RA Yang A., Kaghad M., Wang Y., Gillett			NCBI_TaxID=9606;	Mammalia: Eutheria:	Eukarvota: Metazoa:	OS Homo sapiens (Human)	P63.	DE TA p63 alpha (Tumor protein	01-MAR-2003	01-MAR-2001	01-MAR-2	9H3D4	Q9H3D4
,	- ;	-	Ŀ	5607.1; JOINED.	5607.1; JOINED.	AAG45607.1; JOINED.	AAG45607.1;	NGS TO THE P53 FAMILY.	LOCATION: NUCLEAR (BY SIMILARITY).	EMBL/				EMBL/Ger	in M.G., Harris C.C.;			and dominant-nee	at 3q27-29, encodes multiple products with		Wang Y., Gillett E., Fleming M.D., Dotsch V.,	bMed=9774969;			Catarrhini: Hominidae:	Chordata: Craniata: Vertebrata: Euteleostomi:	-		tein	23, Last	16,		ARY; PRT; 680 AA.	

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InterPro; IPROO
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Genew; HGNC:15979;
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AF124536; AAG45607.1

AF124537; AAG45607.1

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AF075430; AAG62635.1

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; IPR001660; SAM.
)0870; P53; 1.
                                              DAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
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                                                                                                                   GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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Pred. No. 5.2e-28
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MEDLINE=20388515;
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                                                  PQGAVIRAMPYYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
           ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
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     ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                             PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
Nuclear Protein.
SEQUENCE 641 AA; 72019 MW; S
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TISSUE-Skeletal muscle;
TISSUE-Skeletal muscle;
MEDLINE-98324755; PubMod-9662378;
MEDLINE-98324755; PubMod-9662378;
Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
"Cloning and functional analysis of human p51, which functionally resembles p53.";
Nat. Med. 4:839-844(1998).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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P51 isoform TAP63ALPHA (P51B
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tch 99.9%; al Similarity 99.8%; 640; Conservative
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IPR002117; 1
IPR001660; 1
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K., Kawahara C.,
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01-MAY-2000
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SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
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MEDLINE-99018225; PubMed-9799841;
Augustin M., Bamberger C., Paul D., Schmale H.
"Cloning and chromosomal mapping of the human chromosome 3q27 and its murine homolog Ket to Mamm. Genome 9:899-902(1998).

-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY: BELONGS TO THE P53 FAMILY.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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  SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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Pred. No. 2.
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01-JUN-2001 (TrEMBLrel. 1:
01-JUN-2001 (TrEMBLrel. 1:
01-OCT-2002 (TrEMBLrel. 2:
TAL KET alpha protein.
                                                                                                                                                              Interpro; IPRO02117; P53.
Interpro; IPRO01660; SAM.
Pfam; PF00870; P53; 1
PRINTS; PR00388; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STRALN=Wistar; TISSUE=Tongue;
MEDLINE=21363378; PubMed=11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution
                                                                                            PROSITE; PS00348; P53;
Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                               SMART; SM00454; SAM;
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98.1%;
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Score 3353; DB 11;
Pred. No. 1.4e-277;
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Sciurognathi; Muridae;
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    SEQUENCE FROM N.A.
TISSUE-Lingual epithelium;
Schmale H.;
Submitted (APR-2000) to the
-i- SUBCELLULAR LOCATION: N
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Q9JJP6;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
TA2 KET alpha.
                                                                                                 TISSUE-Lingual epithelium;
MEDLINE-97460723; PubMed-9315105;
Schmale H., Bamberger C.;
"A novel protein with strong homo oncogene 15:1363-1367(1997).
[2]
                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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epithelium;
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Murinae; Rat
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PRINTS; PR00388; P535UPPRESSR.
PTODOM; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protetin
SEQUENCE 680 AA; 76760 MW;
                                    O88898
O1-NOV-1998 (7
01-NOV-1998 (7
01-OCT-2002 (7
TA*p63 alpha.
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EMBL; Y10258; CAI
HSSP; P04637; 1YC
InterPro; IPR0010
InterPro; IPR0010
Pfam; PF00870; P:
Mus musculus (Mouse 
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                          640
                                                                                                                                                                                                                                                                                           601
                                                                                                                                                                                                                                                                                                                                   580
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29; Conservative
                                                                                                                                                                                                                                                      DAVRETLRQTISFPFRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                               FEARICACPGRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSQSTQTSEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSENGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001660;
                                                                         3 (TrEMBLrel.
3 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                          PRELIMINARY;
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                (Mouse)
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.5%;
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Pred.
  Craniata;
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Mismatches 5;
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    Vertebrata;
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Best Local :
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Interpro; IPR002117; P53.
Interpro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PfNTS; PR00386; P53SUPPRESSR.
PrODOM; PD002661; P53; 1.
SYART; SM00454; SAM; 1.
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"p63, a pt
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00348; P53; 1. Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: NUCLEAR -i- SIMILARITY: BELONGS TO THE P53 EMBL, AF075436; AAC62641.1; -. HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transactivating, death-inducing, and mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang A., Kaghad M., Gillett E., Caput D., McKeon F.;
                  601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53 homolog at 3q27-29, encodes multiple products with ivating, death-inducing, and dominant-negative activit
                                  GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                                              FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                       DAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                           LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                                                                                                                           DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                                                                                                                                                                               DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPSSTFDAL 120
DAVRFTLRQTISFPPRDEWNDFNFDMDSRRNKQQRIKEEGE
                                                                                                           GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                                    FEARICACPGRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSMQSQSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                   680 AA; 76788 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9774969;
                                                                                                                                                                                                                                                                                                                                                                                                                     98.5%;
98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 3353; D
; Pred. No. 1.5e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8DFF0284F247C68A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleming
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                                                                                                                                                                                                                                                                                                                                                                                                                      .5e-277;
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
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                 641
680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activities.";
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Best Local Sin
Matches 572;
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Q9UBV9;
Q9UBV9;
01-MAY-2000 (TrEMBLrel. 1:
01-MAY-2000 (TrEMBLrel. 1:
01-CCT-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMI ARITY: BELONGS TO THE P53 FAMILY. EMBL; AF075431; AAC62636.1; -. EMBL; AF091627; AAC43038.1; -. EMBL; AF124539; AAG45610.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hagiwara K., McMenamin M.G., Harris C.C.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                       PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1.
                                                                                                                                                                                                                                                                InterPro; IPR002117;
InterPro; IPR001660;
Pfam; PF00870; P53; 1
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MEDLINE-98448095; PubMed-9774969;
MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming
Yang A., Kaghad M., Wang Y., Gillett E., Fleming
Andrews N.C., Caput D., McKeon F.;
"P63, a p53 homolog at 3g27-29, encodes multiple
transactivating, death-inducing, and dominant-neg
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                       Nuclear protein. SEQUENCE 586 A
                                                                                                                                                                                                                             SMART; SM00454;
                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee L.A., Walsh P., Prater Dellavalle R.P., Targoff I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of an autoantigen associated with stomatitis: The CUSP autoantigen is a member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jablonska S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                     ; AF124538;
; P04637; 1Y
              190
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AF124536; AAG45610.1;
AF124537; AAG45610.1;
                                                                                                                                                                                                                                                                                                                                                               AF124531; AAG45610.1;
AF124532; AAG45610.1;
AF124533; AAG45610.1;
AF124533; AAG45610.1;
                                                                                                                                                                                                                                                                                                                                                                                                     AF124530; AAG45610.1; AF124531; AAG45610.1;
                                       75
                                                                                       15
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                                                                                                                                                 Similarity
PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                       TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                    TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                     PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                    PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human).
etazoa; Chordata; Craniata; Vertebrata;
theria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                      1YCS
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                                                                                                                                                                                         AA;
                                                                                                                                                                                                                             SAM;
                                                                                                                                                                                                                                                                                                                AAG45610.1;
                                                                                                                                                                                         65756 MW;
                                                                                                                                                                                                                                                                            P53.
                                                                                                                                                 89.1%; Score 3033; DB 4;
100.0%; Pred. No. 2.6e-250;
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Last annotation update)
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                                                                                                                                                                                         2E2F92ABF1AF8629 CRC64;
                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       des multiple products with
  dominant-negative activities.";
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                                                                                                                                                             Length
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                                                                                                                                       Indels
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                                                                                                                                                                586;
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EMBL; AF116758; AAF43491.1;
EMBL; AF116760; AAF43491.1;
EMBL; AF116760; AAF43491.1;
EMBL; AF116761; AAF43491.1;
EMBL; AF116762; AAF43491.1;
EMBL; AF116762; AAF43491.1;
EMBL; AF116765; AAF43491.1;
EMBL; AF116765; AAF43491.1;
EMBL; AF116765; AAF43491.1;
EMBL; AF116765; AAF43491.1;
EMBL; AF116767; AAF43491.1;
EMBL; AF116767; AAF43491.1;
EMBL; AF116767; AAF43491.1;
EMBL; AF116768; AAF43491.1;
EMBL; AF116769; AAF43491.1;
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01-OCT-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
P51 isoform delNalpha.
                       Prodom; PD002681;
SMART; SM00454; SI
PROSITE; PS00348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neoplasia 1:71-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=20388515; Tani M., Shimizu K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                           PR00386; P53SUPPRESSR
PD002681; P53; 1.
SM00454; SAM; 1.
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K., Kawahara C.,
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Matches 571
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075080;
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                                                           TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
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SEQUENCE FROM N.A.

MEDLINE-98365596; Pubmed-9703973;

SEDOO M., Seki N., Ohira M., Sugano S., Watanabe M.,

Tanaka T., Shinkai Y., Kato H.;

"A second p53-related protein, p73L, with high homolo
Biochem. Biophys. Res. Commun. 248.603-607(1998).

-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE P53 FAMILY.

REMBL; AB010153; BAA32433.1; -.

RESEP; P04637; 1YCS.
                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
IPR002117;
IPR001660;
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                                                                                                                                                                                                                                                                               Chordata;
Primates;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
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p73.";

Tachibana to p73.";

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SORPORT

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Best Local Similarity
Matches 569; Conserv
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089097;
01-NOV-1998 (TrEMBLrel. (
01-NOV-1998 (TrEMBLrel. (
01-OCT-2002 (TrEMBLrel. 2
DN P63 alpha.
TRP63 OR P73H.
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PRINTS; PR00386; P53SUPPI
PRODOM; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PR0STTE; PS00348; P53; 1
Nuclear protetin.
SEQUENCE 586 AA; 65734
SEQUENCE FROM N.A.

MEDLINE=98448095; PubMed=9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., A
Caput D., McKeon F.;

"p63, a p53 homolog at 3q27-29; encodes multiple products
transactivating, death-inducing, and dominant-negative act
                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBL_TaxID=10090;
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Pred. No. 7
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Best Local Similarity
Matches 563; Conserv
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EMBL; AB010152; BAA32432.1; -.
HSSP; P04637; TYCS.
MGD; MGI:1330810; Trp63.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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Nuclear protein.
SEQUENCE 586 AA; 657
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Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tac
Senoo M., Seki N., Ohira M., Sugano S.,
Tanaka T., Shinkat Y., Kato H.;
"A second p53-related protein, p73L, with high homology
"A second p53-related protein, p73L, with high homology
Biochem. Biophys. Res. Commun. 248:603-607(1998).
-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. SMART; SM00454; SAM; 1.
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 PRELIMINARY;
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Pred. No. 4.5e-247;
 PRT;
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Matches 562
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01-JUN-2001 (TrEMBLrel.:
01-JUN-2001 (TrEMBLrel.:
01-OCT-2002 (TrEMBLrel.:
DN KET alpha protein.
P63.
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Bamberger C., Schmale H •
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InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
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EMBL; AJ277447; CAC37099.1;
HSSP; P04637; 1YCS.
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ants.";
Lett. 501:121-126(2001).
Communication: NUCLEAR (
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 TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                             IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
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                   IPEQFRHAIWKGILDHRQLHDFSSPPHLLRTPSGASTVSVGSSETRGERVIDAVRFTLRQ
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Pred. No. 9.9e
5; Mismatches
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3 FAMILY.
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RESULT 12

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Best Local S
Matches 548
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Mech. Dev. 100:105-108(2001).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; ABA045224; BAB20631.1; -.
HSSP; P04637, 1YCS.
InterPro; IPR00111; P53.
InterPro; IPR001660; SAM.
Pfam; PF0870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9DEC7 PRELIMINARY;
Q9DEC7;
01-MAR-2001 (TIEMBLIE1. 1
01-MAR-2001 (TIEMBLIE1. 1
01-OCT-2002 (TIEMBLIE1. 2
DN p63 alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein.
SEQUENCE 582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
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431
                                           490
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548; Conserv
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                                                                                GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                                              PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                       LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
                                                                                                                                                                                                                                                                  GRDRKADEDSIRKQQVSDSTKNGDA----FRQGTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                       PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                               PVYKKAGHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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95.8%;
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Last sequence up
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Best Local S
Matches 511
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EMBL;
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EMBL;
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EMBL;
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01-OCT-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
P51 1soform TAp63beta.
                                                                                                                                                                                                                                                             PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20388515;
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                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                             L; AF116769; AAF43488.1; JOINED.
L; AF116757; AAF43488.1; JOINED.
L; AF116759; AAF43488.1; JOINED.
L; AF116760; AAF43488.1; JOINED.
L; AF116761; AAF43488.1; JOINED.
L; AF116762; AAF43488.1; JOINED.
L; AF116763; AAF43488.1; JOINED.
L; AF116754; AAF43488.1; JOINED.
L; AF116755; AAF43488.1; JOINED.
L; AF116756; AAF43488.1; JOINED.
L; AF116766; AAF43488.1; JOINED.
L; AF116766; AAF43488.1; JOINED.
L; AF1167674; AAF43488.1; JOINED.
L; AF116766; AAF43488.1; JOINED.
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                                                                          SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                     DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                 PQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                              SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP1QIKVMTPP
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ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                    PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                         DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPEQFRHAIWKGILDHRQLHDFSSPPHLLRTPSGASTVSVGSSETRGERVIDAVRFTLRQ
                                                                                                                                                                                                                                                                                                          IPR002117; P53.
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                                                                                                                                                                                                                                          516
                                                                                                                                                                                               79.9%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                             P53;
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K., Kawahara C., Kohno
                                                                                                                                                                                                                                          57598 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates;
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15,
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                        Score 2722; DB 4;
Pred. No. 7.9e-224;
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Catarrhini;
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                                                                                                                                                                                               Mismatches
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 Query Match
Best Local Sim
Matches 511;
                                                Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 555 AA; 62433 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9H3D3 PRELIMINARY;
O9H3D3; Q9UD27;
01-MAR-2001 (TIEMBLIEL 1
01-MAR-2001 (TIEMBLIEL 1
01-OCT-2002 (TIEMBLIEL 2
                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: N
-!- SIMILARITY: BELONGS TO
EMBL; AF124539; AAG45608.1;
EMBL; AF124528; AAG45608.1;
EMBL; AF124529; AAG45608.1;
                                                                                                                                                           EMBL;
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EMBL;
EMBL;
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MEDLINE=98448095; PubMed=9774969;
Yang A., Kaghad M., Wang Y., Gillett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                    EMBL; AF075432; AA(HSSP; P04637; 1YCS
                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                        Hagiwara
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                           transactivating, death-ind Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                Andrews N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TA p63 beta
                                                                                                                                               L; AF124528; AAG45608.1; JOINED.
L; AF124529; AAG45608.1; JOINED.
L; AF124531; AAG45608.1; JOINED.
L; AF124532; AAG45608.1; JOINED.
L; AF124533; AAG45608.1; JOINED.
L; AF124534; AAG45608.1; JOINED.
L; AF124536; AAG45608.1; JOINED.
L; AF124536; AAG45608.1; JOINED.
L; AF124536; AAG45608.1; JOINED.
L; AF124537; AAG45608.1; JOINED.
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              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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1 (TrEMBLrel. 16,
2 (TrEMBLrel. 22,
79.9%; S llarity 100.0%; Conservative 0;
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NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                   THE P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation updat
Score 2722; DB 4;
Pred. No. 8.7e-224;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Matches 503
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-!- SIMILARITY: BELONGS TO THE PI
EMBL; AJ277452; ČAC37104.1; -.
HSSP; P04637; 1YCS;
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
Drivers Decorations of the process of the proces
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099JD7;
01-JUN-2001 (TIEMBLIEL 1
01-JUN-2001 (TIEMBLIEL 1
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                                                                                                                                                                 PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PR0SITE; PS00348; P53; 1.
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FEBS Lett. 501:121-126(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat),
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TISSUE-Tongue;
MEDLINE-21363378; PubMed-11470269;
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Search completed: August 7, 2003, 09:51:37
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Maximum Match 100%
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CC which demonstrate certain sequence identity to known tumous conserved between p73 and p53, and from cC intron-exon organisation is conserved between p73 and p53, and from cC intron-exon organisation is conserved between p73 and p53, and from cC identify new members of this gene family using a pCR-based strategy cC of amplifying 2 exons in a conserved domain and their intervening cC intron. The human p53 gene was localised to chromosomal position cC 3q27-29. At least 6 different isotypes exist. Splice variants cC differing at the C-terminus have been designated as alpha, beta and cC gamma forms, while p63 members differing in the N-terminus are cC designated as deltaN and TA forms, where the deltaN form lacks the ctransactivated as deltaN and TA forms, where the deltaN form lacks the chuman and mouse tissue. It demonstrates remarkably divergent cativities, such as the ability to transactivate p53 reporter genes cC and induce apoptosis. Cessation or down-regulation of p63 expression cC differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. CC cachexia) and neuronal differentiation and related degenerative cC disorders. p63 polypeptides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to concleaving the production and diagnosis, and in the production of colored to a detection and diagnosis, and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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SPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVRIWQV 516
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Pred. No. 2.2e-226;
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DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL

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                                                                                     Best Local Similarity Matches 516; Conserv
                                                                                                                                                                         comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
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10-JAN-2000;
22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                        This invention describes a novel isolated polypeptide (I) which
                                                                                                                                                                                                                                                                                                              Disclosure; Page 255-256; 261pp; English.
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                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide comprising an immunogenic portion of a protein is used for detecting and monitoring progression of
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17-DEC-1999;
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vaccine; detection.
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2000US-0510376
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99US-0476496
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Pred. No. 2.2e-226;
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                                                                 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                     Chromosome aberration; oncogenic fusion protein; cancer; oncogen proliferative disease; cellular protein isoform; heat shock prot HSP-90; rheumatoid arthritis; cancer; haematopoletic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CMI acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarc
      The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous
                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                              01-MAR-2001; 2001US-272751P
                                                                                                                                                                             01-MAR-2002; 2002WO-US06518
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                                          Page 349-351; 389pp; English.
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               Human; lung cancer;
                                  Human
                                                   07-OCT-2002
                                                                   ABP61915;
                                                                                   ABP61915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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les 516; Conserv
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                                                                                   standard;
                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                  (first
                                 associated
                                                                                   Protein;
                                                  entry)
               lung tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                            100
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CC protein or cellular protein isoforms (II) dependent on heat shock CC protein (HSP)-90, or selectively treating cells expressing (II) CC involving administering HSP90-inhibitor. The method is useful for CC involving genetically-defined disease with chromosomal aberration yielding CC oncogenic fusion protein, treating cancerous cells containing fusion CC protein in heterogeneous cell population, treating proliferative disease CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or CC possible of the collectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful CC protein isoform in a patient heterozygous for (II). The method is useful CC protein isoform myeloid leukaemia (CML), APL, AML, NHL and CMML, CC or a disease characterised by a solid tumour such as papillary thyroid CC arcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and CC synovial sarcoma. The method is also useful for treating viral for contents of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV
                                                                                            GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                                                                                                                                 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                                                                                                                                                                                                       FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQGAVIRAMPYYKKAEHYTEYVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSDLSDPMWPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                                                                                                                                                                       FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                               ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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2.2e-226;
2s 0;
   516
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AA

protein sequence

SEQ

IJ

NO:344.

cytostatic;

therapy; vaccine

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                                                                                                                                                                                                                                                                                                                                                   The present invention describes isolated human lung carcinoma polynucleotides (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for a cancer in a patient, by cotaining a biological sample from the patient, contacting the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the coligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to confide the presence or absence of a cancer such as lung cancer.

CC AB092145 to AB092486 and ABP61866 to ABP6192 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 516
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07-MAY-2001;
28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel lung carcinoma polynucleotide sequences and polypeptides ence by the polynucleotides, useful in pharmaceutical compositions such vaccines and as markers to indicate the presence of lung cancer -
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carter D,
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516; Conserv
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                                                                                                                                             Wang A, S)
PD, Fanger
           FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                            PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                                                                               MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                             PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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Watanabe Y,
                                                                                                                                                                                                                                                                                                                                                   516
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; 2001US-0850716.
; 2001US-0897778.
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US47576.
                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / YAW, Li SX, Kalos MD, Henders
Retter MW, Durham M, Fanger GR,
Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381pp;
                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                             Score 2751; DB 23; Pred. No. 2.2e-226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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                                                                                                                                                                                                                                                                                                                         516;
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360
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S

MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ

Query Match Best Local s Matches 516

Match 100.0%; Local Similarity 100.0%; les 516; Conservative

0,

Score 2751; DB 23; Pred. No. 2.2e-226; Mismatches 0;

Indels Length

Gaps

60

516; 0

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                                                                                                                                                                                                                                                                                                       21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
                             The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                      Wang T,
McNeill
Sequence
                                                                                                                                                                                          N-PSDB;
                                                                                                                                   Example 2; Page 327-328; 374pp; English.
                                                                                                                                                        Polynucleotides encoding lung lung cancer or stimulating an
                                                                                                                                                                                                                                                                                              07-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                  28-JUN-2000;
02-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
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                                                                                                                                                                                                                                                                       (CORI-)
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)B; ABL49252.
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PD,
k TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lung tumour;
                                                                                                                                                                                                                                                                       CORIXA CORP.
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 516
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Carter D, Watan
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2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0685696.
2000US-0735705.
2001US-0850716.
                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US21065
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 ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                         tumor polypeptides,
immune response -
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, Marnerakis M,
Y, Peckham DW;
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Fanger GF
                                                                                                   and immunostimulant
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                                                                                                                                                                                                    Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform, heat shock protein 90 HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
Treating genetically-defined disease associated with aberrations yielding oncogenic fusion proteins, e.g. \,
                                                                                                01-MAR-2001;
                                                                                                                     01-MAR-2002;
                                                                                                                                          12-SEP-2002
                                                                                                                                                               WO200269900-A2
                                                                                                                                                                                     Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90 inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding concogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. cellular protein isoform dependent on heat shock protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as Tor B cell lymphoma, chronic myeloid leukaemia (CMI). All, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral
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Matches 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous
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                                                                                                                    FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                       SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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                SPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVRIWQV
                                                                        GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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Matches 511;
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suppression;
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                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            AAZ25771
                                           PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                  SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                           DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                        ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                       SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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Pred. No. 9.2e-224;
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                  The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the cintron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isotypes exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are transactivation domain. The present sequence represents human p63 was detected in a variety of human and monker titles of the present sequence and variety of human and monker titles of the present sequence represents human p63 was detected in a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell regulatory protein; p63; huTAp63 alpha; TAp63 alpha; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
                                                                                                                                                                                                                                                 Claim
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15-OCT-1997;
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DB; AAX58572.
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97US-0062076.
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        demonstrates remarkably
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                                                                                                              Lung
vacci
                                        WO200061612-A2
                                                                                                                                                                 Human
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                                                                                                                             tumor;
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.2e-224;
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
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                                                     GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                                             LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
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2000US-0510376.
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Pred. No. 9.2e-224;
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cancer tumor

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SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimera gene of the p53 family, useful for gene therapy, and treatment of cancer, comprises a transcription activating region and a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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PQGAVIRAMPYYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                DSDLSDPMWPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II)

involving administering

HSP90-inhibitor.

Disclosure;

Paeg

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                  Chromosome aberration; oncogenic fusion protein; cancer; oncogen proliferative disease; cellular protein isoform; heat shock proliferative disease; cellular protein isoform; heat shock proliferative disease; callular protein isoform; heat shock proliferative disease; cellular protein disease properties of the proliferation of the province of the pr
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                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                          641
  ALL; APL;
  NHL;
                                                                                                                       cancer; oncogene;
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DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL

MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ

Query Match Best Local Matches 51

Similarity

98.9%;

Score 2722; DB 23; Pred. No. 9.2e-224;

Conservative

0;

Mismatches

0

Length Indels

Gaps

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associated with chromosomal aberrations yielding oncogenic fusion corrections (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating paroliferative diseases associated with mutant cell protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) cellular protein (HSP)-90, or selectively treating cells expressing (II) concogenic fusion protein, treating cancerous cells containing fusion protein, treating cancerous cells containing fusion protein in protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. CC postein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoletic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and curroutal escretain cancer and contains a papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                               The
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
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rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                            synovial sarcoma. The method is also useful for treating viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aberrations
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                                          infections. This is the amino acid sequence of a human oncogenic
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641
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferations diseases, involves administering an inhibitor of heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosome aberration; oncogenic fusion protein; cancer; oncog proliferative disease; cellular protein isoform; heat shock profise proliferative disease; cellular protein isoform; heat shock profise proliferative disease; cellular protein famoutopoletic disorder; HSP-90; rheumatold arthritis; cancer; haematopoletic disorder; Tcell lymphona; Bcell lymphoma; chronic myelomonocytic leukaemia; Cacute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposa
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
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DB; ABS73334.
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                                                                                                                                                                                                                                                                                                                                                              SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
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                                                                                                                                                                                                           ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                                            PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        641 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.9%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2722;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                 480
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RESULT 14
ABP61910
 12-DEC-2000;
07-MAY-2001;
                                                                          Human;
                                                                                                     07-OCT-2002
                    30-NOV-2001; ,2001WO-US47576
                                  20-JUN-2002
                                                                                       Human lung cancer associated
                                                                                                                               ABP61910
                                                                        lung
                                                                                                                              standard;
2000US-0735705
2001US-0850716
                                                                                                                              Protein;
                                                                         Lung
                                                                                                    entry)
                                                                         tumour;
                                                                                      protein sequence SEQ
                                                                         cytostatic;
                                                                         gene therapy; vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC activity, and can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC a patient and for treating lung cancer in a patient. Oligonucleotides of CC (I) can be used for detecting the presence of a cancer in a patient, by CC obtaining a biological sample from the patient, contacting the sample, an CC comparing the amount of polynucleotide that hybridises to the oligonucleotide and CC comparing the amount of polynucleotide that hybridises to the oligonucleotide contacting the presence of a cancer in the patient. (I) and (II) are useful in CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to contact the presence or absence of a cancer such as lung cancer. CC AB092145 to AB092486 and AB09186 to AB09192 represent sequences used CC in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang T, Wang A, Skeiky YAW,
McNeill PD, Fanger N, Rette
Carter D, Watanabe Y, Peckh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-)
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DB; ABQ92433.
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 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Page 328-329;
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                                                                                                                                                                                                                                                                                                        DSDLSDPMWPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                    MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                        GNSSPELNKMNSMNKLPSVSQLINPQQRNALTETTIPDGMGANIPMMGTHMPMAGDMNGL
                                                                                                LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                                      FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                  SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                                                                                                                                                             ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC
                                                                                                                                                                                                                                                                                                                                                                DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                                                                                                                                                                                                                                                      MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSY
                                                                                                                                         FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     641 AA;
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100.0%;
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Peckham DW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2722; DB 23; Pred. No. 9.2e-224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Durham |
Cai F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kalos MD, Hendersourham M, Fanger GR, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641;
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RESULT 15
ABB74990
ID ABB74
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XX
AB AB74990
ID ABB74
XX
AC ABB74
XX
DT 01-MA
XX
Human
PF 28-JU
PF 28-JU
PF 28-JU
PR 21-NE
PR 15-SE
PR 15-SE
PR 15-SE
PR 15-SE
PR 17-NE
PR 15-NE
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Best Local S
Matches 511
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21-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                   The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL49959 to ABL49300 and ABB74946 to ABB75970 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang T,
McNeill
                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotides encoding lung lung cancer or stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vedvick
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12-DEC-2000;
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DB; ABL49247.
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                                                                                                                                                                              tch 98.9%; S
al Similarity 100.0%;
511; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
                            DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                     \tt MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 321-322; 374pp; English.
                                                                                                                                                                                                                                                                           641
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2000US-0735705.
2001US-0850716.
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2000US-063Q940.
2000US-0643597.
2000US-0662786.
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jer N, R
jer D, W
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Retter MW, 1
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                                                                                                                                                                              Score 2722; DB 23;
Pred. No. 9.2e-224;
0; Mismatches 0;
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immune response -
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, Marnerakis M,
Y, Peckham DW;
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Fanger GR;
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SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP

181 PQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	EGNSHAQYVEDP 240
181 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIF	EGNSHAQYVEDP 240
241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT	ETRDGQVLGRRC 300
241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVI	ETRDGQVLGRRC 300
301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIC	TSIKKRRSPDDE 360
301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIC	TSIKKRRSPDDE 360
361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHI	QKQTSIQSPSSY 420
361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHI	QKQTSIQSPSSY 420
421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPM	THMPMAGDMNGL 480
421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPM	THMPMAGDMNGL 480
481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511	
481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511	

Search completed: August 7, 2003, 09:46:23 Job time: 37.5862 secs

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protein on :

Sequence: Title: Perfect score:

Scoring table:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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2751
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2: //cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: //cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: //cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: //cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: //cgn2_6/ptodata/1/1aa/backfiles1.pep:*
6: //cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
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APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHOI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG OF FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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Matches 516
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GENERAL INFORMATION
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Fanger, Gary R.
Li, Samuel X.
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Kalos, Michael D.
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US-08-047-041A-27
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US-08-347-792-2
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Pred. No. 4e-241;
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Minimum DB Maximum DB

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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FO
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.455CB
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOUTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
TYPE: PRT
ORGANISM: Homo sapiens
US-09-542-615A-344
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Similarity 100.0%;
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  LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSY
                                         FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE
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Kalos, Michael D.
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Pred. No. 4e-241;
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 2101.21.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Wang, Tongton
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Micha-
APPLICANT: Bangur, Chai-
APPLICANT: Hosken, Nance,
APPLICANT: Fanger, Gary
APPLICANT: Li, Samuel X
APPLICANT: Wang, Aijun
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Pred. No. 4e-241;
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; SOFTWARE: FastSEQ for W
SEQ ID NO 339
; LENGTH: 641
; TYDE: PRT
; ORCANISM: Homo sapiens
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CURRENT FILING DATE: 2000-08-21
NUMBER OF EQ ID NOS: 369
CORTRADE: FREEED for Utalian Various 2
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APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
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Fanger, Gary R
Li, Samuel X.
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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA FILE REFERENCE: 210121.455C8

CURRENT APPLICATION NUMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 350

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RESULT 6
US-09-606-421B-339
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; Patent No. 6531315
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US-09-542-615A-339
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SOFTWARE: Fas
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Best Local Similarity 100.
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Fan, Liqun
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Pred. No. 2.4e-238;
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APPLICANT: Fan, Liquing APPLICANT: Kalos, Michael D.
APPLICANT: Hangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: NUCENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DAYE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-606-421B-339
                                                      Sequence 342, Application US/09643597 Patent No. 6426072 GENERAL INFORMATION:
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Best Local
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Fan, Liqun
Kalos, Michael
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Pred. No. 2.4e-238;
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RESULT 8 US-09-542-615A-342

US/09542615A

GENERAL INFORMATION: Sequence 342, Application Patent No. 6518256

APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:

Wang, To...
Wang, To...
Fan, Liqun
Kalos, Michael D.
Kalos, Chaitanya S
Tongur, Chaitanya S

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TITLE OF.

NT: Bangur, Chaitanya NT: Hosken, Nancy A. NT: Fanger, Gary R. F INVENTION: COMPOUNDS

COMPOUNDS

AND

METHODS

THERAPY

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APPLICANT: Hosken, Nancy
APPLICANT: Enger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Menderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION SIGNER: TOUR CANCER
CURRENT APPLICATION SIGNER: SOFTWARE: FRASISEQ FOR WINDOWS Version 3.0
SOFTWARE: FRASISEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                          GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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pred. No. 1.4e-237;
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Garry R.
APPLICANT: L1, Samuel X.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TILE REFERENCE: 210121.455C9
CURRENT APPLICATION UNBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
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US-09-606-421B-342
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US-09-542-615A-342
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 342
LENGTH: 680
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APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
FITTLE OF INVENTION: COMPOSITIONS AND ME
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION UMBER: US/09/643,59
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369

LUNG METHODS CANCER

THE

THERAPY

Skeiky, Yasır A.W Wang, Aijun

SOFTWARE: Fa SEQ ID NO 343 LENGTH: 461

FastSEQ for Windows

Version

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; LENGTH: 680
; TYPE: PRT
; ORGANISM: HOMO :
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SEQ ID NO 342
LENGTH: 680
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APPLICANT:
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Fan, Ligun
                                  Fanger, Gary R. Li, Samuel X.
                                                        Hosken,
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GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: Kalos, Michael D.

APPLICANT: Kalos, Michael D.

APPLICANT: Hosken, Nancy A.

APPLICANT: Hosken, Nancy A.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FO

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA

FILE REFERENCE: 210121.455CB

CURRENT APPLICATION NUMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 350
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                                                                                                                                          ; ORGANISM: Homo sapiens US-09-542-615A-343
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US-09-542-615A-343
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Best Local :
                                                                                                                                                                                                       SEQ ID NO 343
                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                          LENGTH: 461
TYPE: PRT
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                                                                              Conservative
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                                                                                             86.5%;
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                                                                          Score 2379; DB 4; .; Pred. No. 1.9e-207; ...
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRT
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US-09-606-421B-343
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Best Local S
Matches 447
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitan
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
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 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                              PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
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Hosken, Nancy
Fanger, Gary R
Li, Samuel X.
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Bangur, Chaitanya
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100.0%; Pred. No. 1.9e-207;
tive 0; Mismatches 0;
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; SOFTWARE: FastSE
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo s
US-09-643-597-338
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APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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Pred. No. 4e-203;
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
ITITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-542-615A-338
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APPLICANT: Wang, To
APPLICANT: Fan, Lig
APPLICANT: Kalos, M
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APPLICANY: LI, Samuer A.

APPLICANY: Wang, Aljun

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C9

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILLING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 338

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapiens

US-09-606-421B-338
Search completed: August 7, Job time: 16.2345 secs
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chait
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Matches 439;
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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Listing first 45 summaries
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6: /cgn2_6/ptodata/1/pubpaa/US10C_NEW_PUB.pep:*

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2781.719 Million cell updates/sec
Sequence 344, App
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Sequence 339, App
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Sequence 342, App
Sequence 342, App
Sequence 343, App
Sequence 338, App
Sequence 338, App
Sequence 338, App
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11 US-09-860-286 9 15 US-10-274-874-4 15 US-10-160-290-2 15 US-10-160-290-2 15 US-10-16-691-2 15 US-10-076-691-2 15 US-10-078-91-3 15 US-10-038-010-6 10 US-09-68-851-34
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15 US-10-274-874-19
11 US-09-466-396A-15
10 US-09-897-778-152
10 US-09-850-716A-15
9 US-09-735-705-152

ALIGNMENTS

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APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 344

LENGTH: 516

TYPE: PRT

ORGANISM: Homo sapiens
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                                                                       Query Match
Best Local S
Matches 516
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                 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
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Fan, Liqun
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Li, Samuel X.
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Bangur, Chaitanya S.
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                                                                       100.0%; Score 2751; DB 9; ilarity 100.0%; Pred. No. 1.6e-220; Conservative 0; Mismatches 0;
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US-09-850-716A-344
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US-09-850-716A-344
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CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C15
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DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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Pred. No. 1.6e-220;
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APPLICANT: Henderson, Robert A.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C16

CURRENT APPLICATION NUMBER: US/09/897,778

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 344

LENCTH: 516

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US-09-897-778-344
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Matches 516
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APPLICANT: Marne:
APPLICANT: Fange
APPLICANT: Vedvi.
APPLICANT: Carte
APPLICANT: Watan
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Patent No. US2002
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mes 516; Conserv
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APPLICANT: MCNeill, Patricia D.

APPLICANT: Fanger, Neil

FITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI

FITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: U$\( \)9/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSEQ for Windows Version 3.0

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Henderson, Robert A.
McNeill, Patricia D.
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Fan, Liqun
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APPLICANT: Marc W.

APPLICANT: Meneill, Patricia D.

APPLICANT: Metter, Marc W.

FITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455015

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FASCSEQ for Windows Version 3.0

SEQ ID NO 339

SEQ ID NO 339

LENGTH: 641

TYPE: PRT

ORGANISM: Homo sapiens

US-09-850-716A-339
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APPLICANT: Marnerakis, Man
APPLICANT: Fanger, Gary R
APPLICANT: Vedvick, Thomas
APPLICANT: Carter, Darric)
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CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 339
LENGTH: 641
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APPLICANT: Franger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C.
FILE REFERENCE: 210121.455C16
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Pred. No. 5.5e-218;
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CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
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Fanger
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McNeill, Patricia
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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION UNUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
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US-09-807-778-342
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-09-850-716A-342
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TYPE: PRT
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Carter, Darrick
Watanabe, Yoshihiro
Henderson, Robert A.
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Fanger, Gary R.
           Peckham,
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Pred. No. 2.8e-217;
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RESULT 10
US-09-735-705-343
; Sequence 343, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
APPLICANT:
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Skeiky, Yasir A.W.
Henderson, Robert A.
McNeill, Patricia D.
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Fanger, Gary R.
Li, Samuel X.
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INVENTION: f: Fanger,
INVENTION:

COMPOSITIONS AND AND DIAGNOSIS OF

METHODS FOR LUNG CANCER

THE THERAPY

Neil

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; ORGANISM: HOMO US-09-850-716A-343
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US-09-850-716A-343
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                                                                                              NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows
SEQ ID NO 343
LENGTH: 461
                              Query Match
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     Matches
                                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
                                                                                                                                                                                                               APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
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CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/897,778; CURRENT FILING DATE: 2001-06-28; NUMBER OF SEQ ID NOS: 467; SOFTWARE: FRASTSEQ for Windows Version 4.0; SEQ ID NO 343; LENGTH: 461; TYPE: PRT; ORGANISM: Homo sapiens
US-09-897-778-343
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APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Penderson avid W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
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APPLICANT: Marne
APPLICANT: Fange
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                                                                                                                                                          Local Similarity 100 hes 447; Conservative
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Carter, Darrick
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Pred. No. 1.2e-189;
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; APPLICANT: Franger, Neil; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; TILE REFERENCE: 210121.455C14; CURRENT APPLICATION NUMBER: US/09/735,705; CURRENT FILING DATE: 2000-12-12; NUMBER OF SEQ ID NOS: 419; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 338; SEQ ID NO 338; LENGTH: 586
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Pred. No. 1.2e-185;
1; Mismatches 2;
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APPLICANT: MAIOS, Michael D.
APPLICANT: MCNeill, Partricla D.
APPLICANT: MCNeill, Partricla D.
APPLICANT: MCNeill, Partricla D.
APPLICANT: MCNeill, Partricla D.
APPLICANT: MAIC W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: HOMO sapiens
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US-09-850-716A-338
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LSMPSTSHCTPPPPPYPTDCSIV
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                                                                                                 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTS1QSPSSYGNSSPPLNK
                                                                                                               ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLLQKQTSIQSPSSYGNSSPPLNK
                                                                                                                                                                                                                                                                                                                              TDYPGPHSSDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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                                         {\tt MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP}
                                                                                                                                                                                                                 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETYEMLLKIKESLELMQYLPOHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2333; DB 10;
Pred. No. 1.2e-185;
1; Mismatches 2;
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g

435

LSMPSTSHCTPPPPPPPTDCSIV 456

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CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-897-778-338
; Sequence 338, Application US/09897778
parent No. US20020147143A1
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APPLICANT: Wang, Tongtong
APPLICANW: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 84.8%;
Best Local Similarity 99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
                                                                                                                                                                                                                                                              250 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP 309
430 MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 489
                                                                    375
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                                                                                                                                                                                             GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 369
                                                                                                                                                                                                                                                                                                                              PYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
                                                               MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 434
                                                                                                                                 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK 374
                                                                                                                                                    ETYEMILKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2333; DB 10;
Pred. No. 1.2e-185;
1; Mismatches 2;
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Search completed: August 7, 2003, 09:57:07 Job time: 24.0296 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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seq length: 2000000000
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Match
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JH0631
cellular tumor antigen p53 - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JH0631
R;de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A;Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A;Reference number: JH0631; MUID:92210006; PMID:1339362
A;Accession: JH0631.
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118	118.5	118.5	119.5	119.5	119.5	120	120	120	120.5	122	122	122.5	123	125	125
4.3	4.3	4.3	4.3	4.3	4.3	4.4	4.4	4.4	4.4	4.4	4.4	4.5	4.5	4.5	4.5
792	884	513	1819	1706	596	1211	832	561	901	864	864	969	1572	799	724
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T26050	T40690	T41011	T32008	184499	T03908	T42230	S56230	T14792	JC6093	T04518	H85335	T15446	S45251	JH0797	T47149
hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	zinc finger protei	hypothetical prote	AF4 protein - mous		hypothetical prote	dead ringer nuclea	hypothetical prote	hypothetical prote	hypothetical prote	SNF2alpha protein	castor protein - f	hypothetical prote

ALIGNMENTS

Oy 361 LLYLPVRGRETYEMLLKIKESLELMQYLQHTIETYRQQ 399	Qy 309 PGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQ-NTHGIQMTSIKKRRSPDDE	Qy 249 VPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICAC 	Qy 189 MPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVL : : : : :	Qy 129 NTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA	QY 71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS 128	QY 11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATIKIEISMDCIRMQDSDLSDPMWP 70	Query Match 30.8%; Score 847.5; DB 1; Best Local Similarity 45.4%; Pred. No. 1.1e-52; Matches 181; Conservative 61; Mismatches 102;	A; Molecule type: mRNA A; Residues: 1-396 < DEF> A; Residues: 1-396 < DEF> A; Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829 A; Cross-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829 A; Experimental source: liver C; Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive C; Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive C; Superfamily: cellular tumor antigen p53 C; Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho F; 164, 167, 227, 231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F; 395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399 : : : : : : : TYTIOTRGKEKYEMIKKENDSLEFISELVPVADADRYROK 365	THGIQMTSIKKRRSPDDE 360	TLETRDGOVLGRRCFEARICAC 308	RVEGNSHAQYVEDPITGRQSVL 248 :: : RVEGNQRSEYMEDGNTLRHSVL 206	AKTCPIQIKVMTPPPQGAVIRA 188 : : AKTCPVQIVVDHPPPPGAVVRA 147	PYAQPS-STEDALS-PSPAIPS 128 : : : papQPSISTLDTGSPPTSTVPT 87	KIEISMDCIRMQDSDLSDPMWP 70	; Length 396; ; Indels 55; Gaps 10;	49605.1; PID:g213829 ppressor gene, p53, whose inact nding; homotetramer; nucleus; pcys) #status predicted #status predicted

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A29376
cellular tumor antigen p53 - African clawed frog
cellular tumor antigen p53 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29376; S61531; S72313; I51639
R;Soussi, T: de Fromentel, C.C.; Mechall, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding
A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding
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C;Superf
C;Keywor
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F;362/B
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A;Title: Overexpression of wild-type p53 interferes with
A;Reference number: I51639; MUID:94134403; PMID:8302570
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A; Residues: 1-51, 'S', 53-70, 72-293, 295-363
A; Cross-references: EMBL: X77546; NID: g4689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-293, 295-363 <HOE>
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Oncogene 9, 109-120,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-363 <SOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keywords: apoptosis; cell división control; DNA binding; homotetramer; nu;150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
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Best Local :
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                                                                                      R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI
                                                                                                                                                                                                                                                                         LVVVDDDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV 334
                                                                                                                                                          RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR
                                                                                                                                                                                                        EDVNSGRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTIITLETPQGLLLG
                                                                                                                                                                                                                                EDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLG
                                                                                                                                      RRCFEVRVCACPGRDRRTEEDNYTKKRGLKPSGK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQSTQTNEFLSPEVFQHIWDFLEQPI----CSVQPIDLNFVDEPSEDGATNKIEISMDCI 57
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.513; PIDN:CAA54672.1;
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ntenarh, M.; Knoe
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chel, W.
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cellular tumor antigen p53 - bovine
N,Alternate names: tumor-suppressor protein p53
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S51648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; E;161,164,224,280/Binding site: zinc (Cys, His, Cys, Cys) #status predict F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P. Nucleic Acids Res. 16, 11383, 1988
A;Title: Nucleotide sequence of a CDNA encoding the chicken A;Reference number: S02193; MUID:89083584; PMID:3060861
A;Accession: S02193
A;Molecule type: mRNA
A;Residues: 1-367 <S0U>
                                                                                                                                                                                                                                                           R; Dequiedt, F.; Willems, L.; Burny, submitted to the EMBL Data Library, A; Description: Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: nuclear oncoprotein p53
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep_1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S02193
                        A;Cross-references: EMBL:X81704; NID:9602332; PIDN:CAA57348.1; PID:9602333 (;Superfamily: cellular tumor antigen p53 (C;Superfamily: cellular tumor antigen p55 (C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;385/Binding site: phosphoryl-RNA (Ser) (covalent)
                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-386 <DEQ>
                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                        A; Accession: S51648
                                                                                                                                                                                                                                   A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPPQGAVIRAM 189
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Pred. No. 7.7e-47;
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                                                      61 DSDLSDPMWPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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                                                                                                                  2 SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                 Similarity
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SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
                             ----DLFLPQDV-AELLEGPEEALQVSAPAAQEPGTE-----APAPVAPASATPWPL
                                                                                        SQSDMSIELPLSQETFSCLWKLL--PPDDILP-----TTATGSPNSME-----
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                                                                                                                                                26.7%; Score 735; DB 1; 38.3%; Pred. No. 1.1e-44; ative 72; Mismatches 134
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smatches 94;
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C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; E;179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted E;395/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M75144;
A;Experimental source: kidney,
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: JH0633
R;Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A;Title: The cDNA cloning and immunological characterization
A;Reference number: JH0633; MUID:92210007; PMID:1555773
A;Accession: JH0633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: tumor-suppressor protein p53
C;SpecLes: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: JH0633
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A; Residues: 1-396 < LEG>
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RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRE
                                           YEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTITLEDPSGNLLGRNSFEVRICACPG
                                                            YEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPG
                                                                                                     IYKKLQYMTEVVRRCPHHERSSE-GDG-LAPPQHLIRVEGNMHAEYLDDKQTFRHSVVVP
                                                                                                                    VYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVP
                                                                                                                                                              TYQGDYGFRLGFLHSGTAKSYTCTYSPSLNKLFCQLAKTCPVQLWYSSTPPPGTRVRAMA
                                                                                                                                                                                            DYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMP 190
                                                                                                                                                                                                                       SENVAGWLEDPGEALQGSAAAAAPAAPAAEDPVAETPAPVASAPATPWPLSSS--VPSYK
                                                                                                                                                                                                                                                  QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFEVRVCACPGRDRRTEEENFRKKEEHCPELPPGSAKRALPTST----SSSPQQKKKPLD
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                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:g191414;
strain MP1
                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                          Score 719; DB 1;
Pred. No. 1.5e-43;
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A;Molecule type: mRNA
A;Residues: 1-71,'p',73-393 <ZAK>
A;Residues: 1-71,'p',73-393 <ZAK>
A;Cross references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1;
A;Cross references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1;
R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
Mol. Cell. Biol. 5, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for huma A;Reference number: A55060; MUID:88267676; PMID:3894933
A;Accession: A55060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-71, /p',73-393 <BUC2>
A;Residues: 1-71, /p',73-393 <BUC2>
A;Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476
A;Note: this 72-Pro allele was found in both normal and malignant cell lines
R;Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
submitted to the EMBL Data Library, August 1990
A;Reference number: S40773
A;Accession: S40773
                                                                A; Molecule type: mRNA
A; Residues: 1-71,'p',3-272,'H',274-393 <HAR>
A; Residues: 1-71,'p',3-272,'H',274-393 <HAR>
A; Cross-references: GB: K03199; NID: g189478; PIDN: AAA59989.1; PID: g189479
A; Experimental source: clone pR4-2, cell line A431
R; Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.;
MOI. Cell. Biol. 6, 4650-4656, 1986
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C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C;Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; 4905; I58354; I78850; I52681; S60153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Human p53 cellular tumor antigen: A; Reference number: A22837; MUID:85230577; A; Accession: A22837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; R;Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M. EMBO J. 4, 1251-1255, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Isolation and characterization of A; Reference number: $42669; MUID:85126934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; R;Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, EMBO J. 3, 3257-3262, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: A variation in the A; Reference number: JT0436; A; Accession: A43073
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N;Alternate names: cellular phosphoprotein p53
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            A; Title: Molecular basis for heterogeneity A; Reference number: A93086; MUID: 87089826;
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A;Residues: 101-393 <MKI1>
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A;Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-393 <BUC1>
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R;Buchman, V.L.; Chumakov, P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-393 <LAM>
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Cell. Biol. 6, 1379-1385, 1986
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            of the human PMID:3025664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequence and PMID: 4006916
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PMID:6396087
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L.; Benchimol,
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A; Residues: 1-189, 'LLSILSEWKEICVWSIWNTETLFDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA'
A; Cross-references: EMBL: X60010; NID: 9506432; PIDN: CAA42625.1; PID: 9506433
A; Cross-references: EMBL: X60010; NID: 9506432; PIDN: CAA42625.1; PID: 9506433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: clone J6K R;Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H. EMBO J. 10, 2879-2887, 1991 A;Title: p53 is frequently mutated in Burkitt's lymphoma A;Reference number: I38082; MUID:92007731; PMID:1915267 A;Accession: I38082
                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-247, 'Q', 249-393 <F08>
A; Cross-references: EMBL: X60017; NID: g506446;
                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A; Cross-references: EMBL: X60016; NID: g506444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-236,'I',238-393 <F05>
A;Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441
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A; Residues: 1-245, 'T', 247-393 <F04>
A; Cross-references: EMBL:X60013; NID:g506438;
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A; Residues: 66-71, 'P',73-79 <MKI2>
A; Experimental source: clone lambda
A; Note: 72-Cys was also found, and
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A;Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A;Experimental source: clone p53-H-19; transformed hybridoma SV-80 cell line
R;Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, I
Mol. Cell. Biol. 7, 961-963, 1987
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A;Residues: 1-78,'T',80-393 <HAR1>
A;Cross-references: EMBL:M1694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A;Experimental_source: clone p53-H-1, transformed hybridoma SV-80 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; MoLecule type: mRNA A; Residues: 1-247,'Q', 249-393 <F06> A; Residues: 1-247,'Q', 249-393 <F06> A; Cross-references: EMBL: X60015; NID: 9506442; A; Accession: I38088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-71, 'P',
                                      A; Molecule type:
A; Residues: 1-71,
                                                                                                   A; Status: translated from GB/EMBL/DDBJ
                                                                                                                             A; Accession: I38090
                                                                                                                                                                                                                                                        A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: X60012; NID: g506436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-393 <F03>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: I38084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-192, 'R', 194-393 <F02>
A; Cross-references: EMBL: X60011; NID: g506434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-192, 'R', 194-393
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A; Residues: 66-79 < mKI3>
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                                                             mRNA
                                   'P',73-162,'H',164-393
      EMBL:X60018;
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164-393 <F09>
NID:g506448;
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 PMID: 3547088
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      PIDN: CAA42633.1;
                                                                                                                                                                 PIDN:CAA42632.1;
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   PID:g506449
                                                                                                                                                             PID: 9506447
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A;Accession: I38091
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-212,'Q',214-393 <F10>
A;Cross-references: EMBL:X60019; NID:9506450; PIDN:CAA42634.1; PID:9506451
A;Accession: I38092
A;Cross-references: EMBL:X60019; NID:9506452; PIDN:CAA42635.1; PID:9506453
A;Cross-references: EMBL:X60020; NID:9506452; PIDN:CAA42635.1; PID:9506453
A;Cross-references: EMBL:X60020; NID:9506452; PIDN:CAA42635.1; PID:9506453
A;Cross-references: EMBL:X50020; NID:9506452; PIDN:CAA42635.1; PID:9506453
A;Cross-references: EMBL:X50020; NID:9506452; PIDN:CAA42635.1; PID:9506453
A;Cross-references: EMBL:X50020; NID:9506452; PIDN:CAA42635.1; PID:9506453
A;Cross-references: EMBL:X54156; NID:9317726; PMID:1762941
A;Tille: An Alu polymorphism intragenic to the TP53 gene.
A;Reference number: I38093; MUID:92107726; PMID:1762941
A;Reference number: I38093; MUID:92107726; PMID:1762941
A;Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
A;Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
A;Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; NID:935214
A;Tille: D53 GPDE muitations in Gastrifo Cancer metastages and in Gastrifo Cancer
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A;Title: p53 gene mutations in gastric cancer metastases and in A;Reference number: A44905; MUID:92034678; PMID:1933850
A;Accession: A44905
A;Molecule type: DNA
A;Residues: 246-247, 'W', 249-250 <YAM>
A;Residues: 246-247, 'W', 249-250 <YAM>
A;Cross-references: GB:S63157; NID:9237829; PIDN:AAB20140.1; PID A;Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBI A;Note: mutation from a liver metastasis of a gastric cancer R;Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L. Oncogene 6, 1067-1071, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 327-331, 'DQTSFQKENC' <CHO>
A; Residues: 327-331, 'DQTSFQKENC' <CHO>
A; Cross-references: GB:S6666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A; Note: mutant sequence with altered splicing and termination expressed in Mo
R; Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A; Title: Mapping of linear epitopes recognized by monoclonal antibodies with
A; Reference number: S60151; MUID:96133682; PMID:8552047
A; Accession: S60153
                                                                                                                                                                                                                                                                             R;Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A;Title: Nuclear and nucleolar targeting sequences of c-erb-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Alternative splicing of the p53 tumor suppressor A;Reference number: I52681; MUID:94036762; PMID:8221626 A;Accession: I52681
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A; Residues: 274-277, 's', 279-282 <HEN2>
A; Residues: 274-277, 's', 279-282 <HEN2>
A; Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1;
R; Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 244-247, W',249-252 <HEN1>
A;Cross-references: GB:S41969; NID:g1679931; PIDN:AAB19324.1;
A;Accession: I78850
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 3-44 <PET>
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   14
                                                                                                                                                                                  Similarity
                                                                LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                  26.1%;
                                                                                                                                        Score 718; DB 1;
Pred. No. 1.7e-43;
9; Mismatches 132;
NNVLSPLPSQAMDDLMLSPDDIEQWFTE--DP---
                                                                                                                                                                                                                Length 393;
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NCBIP:63158)
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A;Status: not compared with conceptual translation
A;Rolecule type: mRNA
A;Residues: 1-134,'V',136-390 <CHU>
R;Zakut-Houri, R; Oren, M; Bienz, B; Lavie, V; Hazum, S; (Nature 306, 594-597, 1983)
A;Title: A single gene and a pseudogene for the cellular tumous
A;Reference number: A02684; MUID:84068204; PMID:6646235
A;Recession: A02684
A;Molecule type: mRNA
A;Residues: 1-159,'H',161-167,'G',169-233,'I',235-390 <ZAK>
A;Cross-references: GB:X01237; GB:K01700; NID:g53575
A;Cross-references: GB:X01237; GB:K01700; NID:g53575
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat
Mol. Cell. Biol. 6, 3232-3239, 1986
A;Title: Immunologically distinct p53 molecules generated by al
A;Reference number: S38822; MUID:87064640; PMID:3023970
A;Accession: S38822
                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-390 <ARAI>
A; Cross-references: EMBL:M13872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioorg. Khim. 13, 1691-1694, 1987
A; Title: Primary structure of DNA complementary to murine A; Reference number: S06336; MUID:88221682; PMID:3329909
A; Accession: S06336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-134,'V',136-390 <BIE>
A;Cross-references: GB:X00876; NID:g871420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular A;Reference number: A22739; MUID:85027173; PMID:6092064
A;Accession: A22739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cellular tumor antigen p53 - mouse
N;Alternate names: oncoprotein p53
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
                                            A; Molecule type: mRNA
A; Residues: 1-167, 'G', 169-233, 'I', 235-390
                                                                                                           A; Accession: S38823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Chumakov, P.M.
                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 GPDS 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVC
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EMBL:M13873
D.; Yokota,
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                                                                                                                                  NID:g200198;
Wolf, D.; Brill,
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                                                       <ARA2>
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                                                                                                                                  PIDN:AAA39881.1;
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Shohat,
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                                                                                                                                  PID:g200199
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Rotter,
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F;719,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F;389/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;99-289/Domain: DNA-binding core #status predicted <DBC>
F;108-121/Region: L1 loop
F;114-139/Region: conserved region II
F;160-192/Region: L2 loop
F;168-178/Region: conserved region III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-47,'R',49-78,'OW',82-390 <RES>
A;Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571
C;Comment: This DNA-binding protein plays an essential role in the regulation of cell di C;Comment: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-turn; Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein; F;1-44/Domain: transcription activation #status predicted <TRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-167, 'G', '169-390 <ARA3>
A; Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1;
R; Jenkins, J.R.; Rudge, K.; Redmond, S.; Wadde-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
A; Title: Cloning and expression analysis of full length mouse careful commber: 148703; MUID:84272240; PMID:6379601
A; Accession: 148703
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F;233-248/Region: L3 loop
F;267-283/Region: conserved region V
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A; Residues: 1-47, 'R', 49-78, 'QW', 82-390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                           RDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTS
                                                                                                                                                                                                                                                                       NLYPEYLEDROTFRHSVVVPYEPPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTITLED
                                                                                                                                                                                                                                                                                            NSHAQYYEDPITGRQSYLVPYEPPQVGTEETTVLYNFMCNSSCVGGMNRRPILLIVTLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PAPATPWPLSSFVPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---MDDLLLPQ-----DVEEFFEGPSEALRVSGAPAAQDPVTETPGPVA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA
                                           QQQQQQHQHLLQKQTSIQS
                                                                                      PQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---AHATEESGDSRAHSSYLKTKK 370
                                                                                                                                 IKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIE--
                                                                                                                                                                            SSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPELPPGSAKRALPTCT---SASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 171
GOSTSRHKKTMVKKVGPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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38.0%;
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A;Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; F;176,79,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predict F;392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellular tumor antigen p53 - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S06594
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A; Residues: 1-393 < RIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Rigaudy, P.; Eckhart, W. Nucleic Acids Res. 17, 8375,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Nucleotide sequence of a cDNA encoding the monkey A; Reference number: S06594; MUID:90045967; PMID:2530498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S06594
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Best Local
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                                 VRGRETYEMLLKIKESLEL
                                                                                            ACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDELLYLP
                                                                                                                                               VLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARIC
                                                                                                                                                                                                                         RAMAIYKQSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGNLRVEYSDDRNTFRHS
                                                                                                                                                                                                                                             RAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQS 246
                                                                                                                                                                                                                                                                                                                                                                                              QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSP----SPAI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                        ACPGRDRRTEEENFRKKGEPCHELPPGSTKRALPNNT--
                                                                                                                                                                                                                                                                                                                                     PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSQETFSDLWKLLPE-----NNVLSPLPSQAVDDLMLSPD------DLA--QW-
IRGRERFEMFRELNEALEL
                                                                                                                                                                                                                                                                                                PSQKTYHGSYGFRLGFLHSGTAKSVTCTYSPDLNKMFCQLAKTCPVQLWVDSTPPPGSRV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                          --LTEDPGPDEAPRMSEAAPH--MAPTP-AAPTPAAPAPAPSWPLSSSV 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 714.5; DB
Pred. No. 3e-43;
63; Mismatches 1:
35C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113;
                                                                        -SSSPQPKKKPLDGEYFTLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393;
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RESULT S38824 10

13-Jan-1995 #text_change

23-Jul-1999

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cellular tumor antigen p53, minor splice form - mouse c;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_c C;Accession: S38824; S35478
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; S Moll. Cell. Biol. 6, 3232-3239, 1986
A;Title: Immunologically distinct p53 molecules generated γď alternative splicing O.; Rotter,

A; Reference number: S38822; MUID: 87064640; PMID: 3023970 A; Accession: S38824

A; Molecule type: mRNA A; Residues: 1-381 <ARA>

A; Cross-references: GB:M13874; NID:g200202; PIDN: AAA39883.1; PID:g200203

R:Han, K.A.: Kulesz-Martin, M.F. Nucleic Acids Res. 20, 1979-1918, 1992 A;Title: Alternatively spliced p53 RNA in A;Reference number: S35478; MUID:92253421; A;Status: nucleic acid A;Molecule type: mRNA A; Accession: S35478 sequence not shown; transformed and PMID:1579500 translation not shown cells of different

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C;Comment: This protein is a multimer, it plays the central role in a complex DNA dam iption, and recombination by protein/protein interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVR 367
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                                                                                                                                                                                                                                                                     68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor suppressor p53 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Bate: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C;Accession: JCG193
R;Le Goas, F; May, P; Ronco, P.; de Fromentel, C.C.
Gene 185, 169-173, 1997
A;Title: CDNA cloning and immunological characterization of rabbit p53.
A;Reference number: JCG193; MUID:97208869; PMID:9055811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X90592; NID:q1532043; PIDN:CAA62216.1; PID:g1532044
                                                                                                                                                                                                                                                                                               14 LSQETFSDLWKLL------PPNNVLSTLPSSDS------IEELFLSENVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 WPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIP
                                                                                                                                                                                                                                                                                                                                                                                         53 WLEDSGGAL----QGVAAAAAST----AEDPVTETPAPVASAPATPWPLSSS--VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL-SPSPA----
                                                                                                                                                                                                                                                                     11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 AMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                            43;
                                                                                                                                                                                  Length 393;
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                                                                                                                                                                                    DB 2;
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40.7%; Pred. No. 3.5e-42;
ive 59; Mismatches 111;
                                                                                                                                                                                                                            61; Mismatches 116;
                                                                                                                                                                                  25.6%; Score 703.5; DB 2 llarity 41.6%; Pred. No. 1.8e-42; Conservative 61; Mismatches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53
                                                                                                                          cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: p53
C;Superfamily: cellular tumor antigen
C;Keywords: tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | ::| ::|||
334 GHERFKMFQELNEALEL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 GRETYEMLLKIKESLEL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.79
Matches 156; Conservative
                                                                                                  A,Gene: p53
C,Superfamily: cellular t
C,Keywords: liver; tumor
                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-391 <LEA>
A; Residues: 1-393 <LEE>
                                                                                                                                                                                                                          157;
                                                                                                                                                                                                                                                                                                                                                                                                                                128
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                                                                                                                                                                                    Query Match
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Matches
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                                                            규
                                                                      s not known.
C'Superfamily: callular tumor antigen p53
C'Keywords: alternative splicing; phosphoprotein; zinc
F;1-44/Domain: transcription activation #status predicted <TRA>
F;16-26/Region: conserved region I
F;108-121/Region: conserved region II
F;108-121/Region: conserved region II
F;108-121/Region: conserved region II
F;108-121/Region: conserved region II
F;108-121/Region: conserved region IV
F;231-252/Region: conserved region IV
F;331-357/Region: conserved region V
F;313-319/Region: conserved region V
F;313-319/Region: nuclear location signal
F;313-315/Region: tonserved region V
F;313-315/Region: tonserved region V
F;313-319/Region: done in the phosphate (Ser) (covalent) #status predicted
F;7,9,12.18,23,37/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
               A;Cross-references: EMBL:M13874; NID:9200202; PIDN:AAA39883.1; PID:9200203
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
C;Comment: This sequence, produced by alternative splicing of the tenth intron, lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLET 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 RDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 IKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIE-----TYRQQQQQQH 404
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09-May-1997 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ---MDDLLLPQ-----DVEEFFEGPSEALRVSGAPAAQDPVTETPGPVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6%; Score 703.5; DB 2; Length 381; 38.3%; Pred. No. 1.8e-42;
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Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster
A;Title: Cloning and characterization of Chinese hamster
A;Reference number: JC6176; MUID:97183659; PMID:9031625
A;Contents: liver
A;Accession: JC6176
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor suppressor protein p53 - Chinese hamster
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C;Date: 11-Apr-1997 #sequence_revision
C;Accession: JC6176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164; Conservative
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A; Molecule type: DNA
A; Residues: 1-1520 (HENN-
A; Residues: 1-1520 (HENN-
A; Cross-references: GB:M18402; NID:g158598; PIDN:AAA28934.1; PID:g158600
A; Cross-references: GB:M18402; NID:g158598; PIDN:AAA28934.1; PID:g158600
R; Hoffmann, F.M.; Fresco, L.D.; Hoffman-Falk, H.; Shilo, B.Z.
Cell 35, 393-401, 1983
Cell 35, 393-401, 1983
A; Fitle: Nucleotide sequences of the Drosophila src and abl homologs: conservation an A; Reference number: A00628; MUID:84082064; PMID:6317185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Henkemeyer, M.J.; Bennett, R.L.; Gertler, F.B.; Hoffmann, F.M.
Mol. Cell. Biol. 8, 843-853, 1988
A;Title: DNA sequence, structure, and tyrosine kinase activity of the Drosophila mela
A;Reference number: A28128; MUID:88174728; PMID:2832740
A;Accession: A28128
  A;Introns: 30/3; 55/1; 200/2; 299/2; 327/2; 369/3; 589/3; 860/1; 986/1; 1278/1; 1547/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-tyrosine kinase (EC 2.7.1.112) abl - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                            .088 -SSAAVQSQHPMTAQSVT-PMASHIVPVAAPVPVPTFFTIPPPVPPPPPT---ATSTQSQ 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1224 -- DMDEVEERR--NIRRGGYRPPPFHNGTDMMERDMERRDHSMMRPRPNHPLLQMDTAP 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                  1028 KMKQKTQTSDDLEEPSISEQTLNGAEVPSRSNLDFSRPPIFSQQSAAPHVVTASMDVPS 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1280 PONGSDP-----PQPSESCPAPPKNSSKKRNNRRGNRRNTNEHIQANHEDSDSFSTSR 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 PQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPGRDR 313
                                                                                                                                                                                                                                                                                                                                                                                     SMDQQIQNGSSSTSPYNTDHAQNSVTAPS----PYAQPSSTFDALSPSP-AIPSNTDYPG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 PHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAMPVYKK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 AEHVTEVVKRCPNHELSREFNEGQIAP-PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP 253
                                                                                                                                                                                                                     920 QQTQENEEKETWKKDSRASISPK------ICSKDAEDATSEAVNHSTPSTSEDL 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 PVRGRETYEMLLKIKESLELMQYLPQHTIE---TYRQQQQQQQQHQHLLQKQTSIQSPSSYG 421
                                                                                                                                                               3 QSTQTNE-----NFVDEPSEDGHIWDFLEQPICSVQPIDL-----NFVDEPSEDG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Drosophila melanogaster
C;Date: 15-Nov-1984,#sequence_revision 30-Sep-1989 #text_change 11-Jun-1999
C;Accession: A28128; A00628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTPDGMGANIPMMGTHMPMAGDMNGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 KADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKK-----RRSPDDELLYL----
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A;Introns: 112/1; 130/1; 310/2; 449/1; 644/3; 735/1; 775/2; 805/1; 1350/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A;Residues: 'A',375,'AQ',378-644,'VGDV' <HOF>
A;Cross-references: GB:K01042; NID:9157175; PIDN:AAA28443.1; PID:9157176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1143 QPQFLEGLGMTDNEIVADAIRRGMVAPIPQELLMGSGPGHIRDRSQPAL-TASVL---
                                                          Length 1621;
                                                                                                             Indels
                                                                                                                                                                                                                                                                       46 ATNKIEISMDCIR------MQDSDLSD----
                                                  h Similarity 19.6%; Pred. No. 0.069; 11; Conservative 69; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1378 P----PPPLFSPSMILPPPPPLPSE 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 PTQALPPPLSMPSTSHCTPPPPYPTD 507
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                                                                              Local Simi
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1621 <-JOH>
A; CTOSS-references: EMBL:AF003386; NID:g2088833; PID:g2088843; PIDN:AAB54259.1; GSPDB:GN
A; Experimental source: strain Bristol N2; clone F59E12
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R;Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, Anticancer Res. 14, 2039-2046, 1994
A;Title: The canine p53 gene is subject to somatic mutations in thypoid carcinoma. A;Reference number: I46226; MUID:95150524; PMID:7847847
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                                                                                                       QGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPI 241
                                                                                                                                      194 KAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP 253
----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP 181
                                                                                                                                                                                                               TGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF 301
                                                                                                                                                                                                                                                                                                                          EARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDEL 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F59E12.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change,20-Sep-1999 C;Accession: T12564 R;Johnson, D. Submitted to the EMBL Data Library, May 1997 A;Description: The sequence of C. elegans cosmid F59E12. A;Reference number: 218318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cellular tumor antigen p53 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
                                                                                                                                                                                                                                              208 TFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTITLEDSSGNLLGRNSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
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A;Molecule type: DNA
A;Residues: 1-77 <DEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: p53
A;Introns: 24/1; 61/3
C;Superfamily: cellular tumor antigen p53
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                                                                                                                                                                                                                                                                                                                                                                                                                                     LYLPVRGRETYEMLLKIKESLEL 384
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A,Gene: CESP:F59E12.9
A,Map position: 2
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1223

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C; Superfamily: Drosophila protein-tyrosine kinase abl; protein kinase homology; SH2 home C; Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transforming F F; 211-260/Domain: SH3 homology <SH3>
F; 211-360/Domain: SH3 homology <SH2>
F; 346-646/Domain: SH2 homology <SH2>
F; 386-646/Domain: protein kinase homology <KIN>
F; 394-402/Region: protein kinase ATP-binding motif
F; 417/Active site: Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 QHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQ----RNALTPTTIPDG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AGDMNGLSPTQA----LPPPLS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNTDYPGPHSFDVSFQQSSTAKSATWTYSTELK-----KLYCQIAKTCPIQIKVMTPPP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 HAQYVEDPITGRQSVLVPYEPPQV-GTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DG-QVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQN----TH 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 GIQMTSIKKRRSPDDELLY--LPVRGRETYEMLLKIKESLELMOYLPQHTIETYRQQQQQ 402
                                                                                                                                                                                                                                                                                         PICSVQPIDL-----NFVDEPSEDGAINKIEISMDCIRMQDSDLSDPMWPQYINLGLL 78
                                                                                                                                                                                                                                                                                                                                 PGCPPEVYDLMRQCWQWDATDRPTFKSIHHALE-----HMFQESSITEAVEKQ-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 QGAVIRAM -- - PVYKKAEHVTEVVKRC -- -- - PNHELSREFNEGQIAPPSHLIRVEGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ::: | | | || :| | 927 PITVGALDVMNVKQVVNRYGTLP-KGARIGAYLDSLEDSSEAAPALP-------
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                          Query Match 5.1%; Score 140; DB 1; Length 1520; Best Local Similarity 21.2%; Pred. No. 0.13; Matches 120; Conservative 71; Mismatches 230; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                     NSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSP-----
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Search completed: August 7, 2003, 09:53:22 Job time : 19.268 secs

(OT92U) XNAJB 39A9 SIHT

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 7, 2003, 09:32:13; Search time 9.15074 Seconds (without alignments) 2651.784 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-538-106-14
2751
1 MSQSTQTNEFLSPEVFQHIW.........HCTPPPPYPTDCSIVRIWQV 516

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	9100	% Query Match	Length	ä	SUMMARIES	Description
i	atose	March		9	TD.	prion
	1464.5			П	P73_HUMAN	015350 homo sapien
~	1457.5	53		Н	P73_CERAE	
m	847.5	30		Н	P53_ONCMY	P25035 oncorhynchu
4	819.5	59		7	P53_BARBU	Q9w678 barbus barb
2	805.5	29		7	P53_BRARE	P79734 brachydanio
v	795	28		-	P53_ICTPU	
7	777.5			Ч	P53_XENLA	P07193 xenopus lae
8	176	28		-	P53_TETMU	
6	771	28		٦	P53_PIG	
0	770	28			P53_FELCA	felis
_	764.5	27		-	P53_CHICK	-
N	758.5	27		7	P53_CANFA	canis
13	746.5	27		٦.	P53_ORYLA	oryzi
4	740	56		Н	P53_BOVIN	Q29628 bos taurus
S	738	26		Н	P53_MARMO	O36006 marmota mon
9	735	26		П	P53_RAT	
_	732.5	26		Н	P53_CAVPO	Q9wur6 cavia porce
8	730			Ч	P53_TUPGB	
6	729	56		Н	P53_SHEEP	_
0	719	56		Н	P53_MESAU	_
	718			П	P53_PLAFE	012946 platichthys
~	718	26		-	P53_HUMAN	P04637 homo sapien
m	717	26		-	P53_MOUSE	_
~	715.5	26.0		7	P53_MACFA	P56423 macaca fasc
വ	714.5	26.0		-	P53_CERAE	P13481 cercopithec
9	713.5	25.9		Н	P53_MACMU	
7	710.5	25.8		٦	P53_XIPHE	O57538 xiphophorus
8	709.5	25.8		٦	P53_XIPMA	m
6	707.5	25.7			P53_CRIGR	
_	699.5	25.4	391	Н	P53_RABIT	Q95330 oryctolagus
_	969	25.3	314	П	P53_SPEBE	~
a	689.5	25.1	280	-	P53_HORSE	
m	5	21.5	207	٦		Q29480 equus asinu

	Q9r017 mus musculu Q9nrj4 homo sapien P28478 turnip yell			
ABL_DROME GALY_YEAST	ZAP3_MOUSE TUSP_HUMAN V70K_TYMVC	TLE4_MOUSE	TLE4_HUMAN V7OK_TYMV V7OK_TYMVA	STUA_EMENI KI67_HUMAN
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ALIGNMENTS

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Pfam; PF00536; SAM; 1.
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  DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTENST TO P53. HEMIZYGOSITY IS OBSERVED IN NEUROBLASTOMA AND OLICODENDROGLIOMA. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCTION: NOT INDUCED BY DNA DAMAGE.

DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.
                                                           PHÓSPHORYLATION (ISOFORMS ALPHA AND BETA).
MEDLINE-99318135; PubMed-10391251;
Yuan Z.-M., Shloya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
Kharbanda S., Weichselbaum R., Kufe D.;
"p73 is regulated by tyrosine Kinase c-Abl in the apoptotic response
to DNA damage.";
                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA SUBCELLULAR LOCATION: ALPHA, AND HOMOTYPICALLY.

SUBCELLULAR LOCATION: Nuclear.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOIG-015360-7; Sequence=VSP_006538; ISOIG-015350-7; Sequence=VSP_006538; IISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=015350-3; Sequence=VSP_006540, VSP_006541; Note=The splicing of exon 11 results in a frameshift from the original reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isoi-015350-5; Sequence-VSP_006544, VSP_006545; Note-The splicing of exon 11 results in a frameshift from the original reading frame. The splicing of exon 13 reverts the reading frame to the sequence of isoform Alpha;
                                                                                                                                                                                                                                                                   Ή.
                                                                                                                                                       Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu
Kharbanda S., Weichselbaum R., Kufe D.;
Nature 400:792-792(1999).
                                         Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=015350-4; Sequence=VSP_006542, VSP_006543;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Event-Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=015350-2; Sequence=VSP_006539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=015350-6; Sequence=VSP_006546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=015350-1; Sequence-Displayed;
                                                                                                                                                                                                                           "The emerging p53 gene family.";
J. Natl. Cancer Inst. 91:594-598(1999).
Cell Death Differ. 6:389-390(1999).
                    SEQUENCE FROM N.A. (ISOFORM KAPPA).
                                                                                                                                                                                                         MEDLINE-99217940; PubMed-10203277;
                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 439-506.
                                                                                                                         Nature 399:814-817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Epsilon;
                                                                                                                                                                                                                 Kaelin W.G. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Мате≃Карра;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Zeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Beta;
                                                                                                                                                                                                                                                                                                                                                       PROTEIN.
                                                                                                                                                                                                FUNCTION
                                                                                                                                             ERRATUM
                                rhomas
                                                                                                                                                                                                                                                 101
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SYRWIYWREAUDLKGGBUSYRAQGLASSNAATISIGGGGE
LQRQRVWEAVHFRYHITIPNRGGPGGGDEWAPEFEDLP
DCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MEDIATES OLIGOMERIZATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Activator; DNA-binding; Anti-oncogene;
Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY ABL) (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNTRCRHWVLCGDRGLSRPVLQGPSG (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 601990; -. GO: 0003700; F: transcription factor activity; TAS. GO: 00:0003700; F: transcription of apoptosis by DNA damage; TAS. GO: 00:006298; P: mismatch repair; TAS. InterPro; IPR002117; P53. InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-BINDING (POTENTIAL)
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POLY -GLN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
                                                                                                                                                                                   EMBL; Y11416; CAA72220.1; -. EMBL; Y11416; CAA7221.1; -. EMBL; Y11416; CAA7219.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               AAC61887.1;
AAC61887.1;
AAC61887.1;
                                                                                                                                                                                                                                                     AF077628; AAC61887.1;
AF077616; AAC61887.1;
AF077617; AAC61887.1;
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AAC61887.1;
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AAC61887.1;
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AAD39696.1;
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                                                                                                 IKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSH 233
                                                                                                                                                                                                                        293
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                                                                                                                                                                                                                                                                 QVLGRRCFEARICACPGRDRKADEDSIRKQQV -- SDSTKNGDGTKRFFRQNTHGIQM -- T 349
                                                                                                                                                                                                                                                                                                                                 397
                                                                                                                                                                                                                                                                                                                                                       466
                                                                                                                                                                                                                                                                                                                                                                             452
                                           53
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                                                        MDC1RMQDSDLSDPMWPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                                               SSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQ
                                                                                                                                                                                                                     AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDG
                                                                                                                                                                                                                                 SIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQ
                                                                                                                                                                                                                                                                                                                       KQTSIQSPSSYGNSSPPLNKMN-SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPM
                                                                                                                                                                                                                                                                                                                                                                             W----
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecus aethlops (Green monkey) (Grivet).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                               398 RPSHLQ-PPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGPG-
                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein p73 (p53-like transcription factor) (p53-related
  636;
                                                                                                                                                                                                                                                                                                                                                                                                MGTH---MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
                                                                                                                                                                                                                                                                                                                                                                                                           Length
                     114; Indels
  ä
Score 1464.5; DB Pred. No. 4.1e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑĄ
                     60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
53.2%;
57.4%;
          303; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9XSK8; Q9TSQ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein).
TP73 OR P73.
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Query Match
Best Local 9
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                     Matches
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P73_CERAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; Activator; DNA-binding; Anti-oncogene;
Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
VARSPLIC 495 637 SFTGGGONCIEVERSOGLOGINHAUNLIFEDIGALKIPE
OYRMITHKGLODIKGGHOYGAAAQGLIRSSNAAA, SIGGSG
ELORQRINMBAVHFRYRHITIIPNRGGPGAGPDEWADDGFDL
PDCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 QVLGRRSFEGRICACPGRDRRADEDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 SSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 IKVSAPPPPGTAIRAMPV¥KKAEHVTDIVKRCPNHELGRDFNEGOSAPASHLIRVEGNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVLGRRCFEARICACPGRDRKADEDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 GVKKRRHGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQ-----LLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSQSTQTNEFLSPE---VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI----EIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 MDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 IKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDG
                                                                                                           DOMAIN THAT BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                 CENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                 Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115; Indels
                                                                                 DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId-VSP_006537.
7CB200B919C9C70A CRC64;
                                              ISOId=09XSK8-2; Sequence=vSP_006537;
-!- DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAI BINDING DOMAIN AND A C-TERMINAL OLICOMERIZATION TO THE ABL TYROSINE KINNSE SH3 DOMAIN.
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1457.5; DB Pred. No. 1.2e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61; Mismatches
IsoId=Q9XSK8-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y11419; CAA72224.1; -.
EMBL; Y11419; CAA72225.1; -.
HSSP; O15350; ICOK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002117; P53.
InterPro; IPR001660; SAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00454; SAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 637 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103
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Best Local
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Nuclear protein; Phosphorylation; Apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                     TP53 OR P53
                                                                                                                                                                                                                                                                                                                                       P53_BARBU
Q9W678;
                                                                 88
                                                                                                                                            249
                                                                                                                                                                     207
                                                                                                                                                                                             309
                                                                                                                                                                                                                       267
                                                                                                                                                                                                                                               361
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                                                                                                                                                                                                                                                                                                                             P53_BARBU
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                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformmatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                                                   growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                    MEDLINE-92210006; PubMed-1339362; de Fromentel C.C., Padkel F., Chapus A., Baney C., May P., Soussi T.; "Rainbow trout p53: cDNA cloning and blochemical characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSQESFEDLW----SWV
                                                                                                                                                                                                                                                                                                                        -! - FUNCTION: Acts as a tumor suppressor in many tumor types; induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
842225076545AlC CRC64;
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-binding, Transcription regulation; Activator;
In; Phosphorylation; Apoptosis.
1 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
 511
              BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 396;
 MGTH---MPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                                                                                                                                                                                                                                                                                                                                                                                               expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102; Indels
                                                                                                                                                                                Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
                                                                                                                                                      Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.2e-50
                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.8%; Score 847.5; 45.4%; Pred. No. 6.2
                                                                                         396
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS, PRO0386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSTR. PROSTRE, PS00348; P53; 1. Anti-oncogene; DNA-binding; Transuclear protein; Phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M75145; AAA49605.1; -. PIR; JH0631; JH0631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                            Gene 112:241-245(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325
369
303
395
396 AA;
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID-8022
                                                                                                                 01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181;
                                                                                        P53_ONCMY
P25035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
DOMAIN
                         453
167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                             P53_ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                        188
                                                                                      :|||| | : | ||||||| | | ||| :|| ||| :|| ||| ||| ||| ||| ||| TSDYPGALGFQIRFLQSSTAKSVTCTYSPDLNKLFCQLAKTCPVQIVVDHPPPPGAVVRA 147
                                                                                                                                                                          248
                                                                                                                                                                                                     266
                                                                                                                                                                                                                                                                                                                                                                                                                                      VPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICAC 308
                                                                                                                                                                                                                                                                                                                                                                                                     PGRDRKADEDSIRKQQ---VSDSTKNGDGTKRPFRQ-NTHGIQMTSIKKRRS----PDDE 360
87
                                                                                                                                                                                                                                                                                                                    -----VEFDPSLFEVSATEPAPOPSISTLDTGSPPTSTVPT
                                                           NTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA
                                                                                                                                                                          MPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Barbus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAX and FAS antigen expression, or by repression of Bol-2 expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLUIAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | :||:| |||| | :|||| : :| : |||:
IYTLOIRGKEKYEMLKKFNDSLELSELVPVADADKYRQK 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF071570; AAD34212.1; -.
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
40 GYDNF ---- MMEAPLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barbus barbus (Barbel).
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345
280
272
372
373 AA;
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093379;
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DOMAIN
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SEQUENCE
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AC 0933_I
D7 16-0C
D7 16-0C
D7 26-FE
DE Cellin
GN IP53
GN IP
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                                                                                                                                                                                                                                                                                                                 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 DQ---ETKTLDKIPSANKRSLIKDSTSSVPRPEGSKKAKLSGSSDEEIYTLQVRGKERYE 312
                                                                                                                                                                                                                                                                                                                                                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 QQVSDSTKNGD----GTKRPF-RQNTHGIQMTSIKKRR----SPDDELLYLPVRGRETYE 373
                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                               Winge P.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAA antigen expression, or by repression of Bcl-2 expression (By similarity).
                                                                                                                                                                                                                                                              VLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97344388; PubMed-9200835; Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S., Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S., "Zebrafish (Danjo rerio) P53 tumor suppressor gene: cDNA sequence and expression during embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                            203 KRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTT
                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                  Gaps
                                                       BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
OBE2CF2CEA74C304 CRC64;
TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                          DB 1; Length 369;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P53_BRARE STANDARD; PRT; 373 AA. 019734; 090440; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                87;
                                                                                                                                                                           ; Pred. No. 4.3e-48; 49; Mismatches 87
                BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                        29.8%; Score 819.5; 51.2%; Pred. No. 4.3
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MLKKINDSLELSDVVPPSEMDRYRQK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 MLLKIKESLELMQYLPQHTIETYRQQ 399
                                                                                                                   41233 MW;
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                                                                                                                                                                         Local Similarity 51.2 es 167; Conservative
28
256
329
365
368
                66
298
342
276
368
369 AA;
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                                       DOMAIN
DOMAIN
DOMAIN
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263
                  DNA_BIND
                                                                                                                                                          Query Match
DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
AC7AB724FA6B6IFF CRC64;
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 --TSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; FOULTS, The Anti-Oncogene; DNA-binding; Transcription regurer...

Anti-Oncogene; DNA-binding; Transcription regurer...

Nuclear protein; Phosphorylation; Apoptosis.

TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 373;
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MEDLINE-99071979; PubMed-9854815;
Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.3%; Score 805.5; DB 1
53.9%; Pred. No. 3.8e-47;
iive 42; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
OLIGOMERIZATION.
SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376
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                                                                                                                                                                                                                                                                                                                                                         EMBL: U46693; AAA97408.1; -. HSSP; P04637; ITUP.
ZFIN; ZDB-GENE-990417; P53.
InterPro; IPRO02117; P53.
Pfam; PRO0870; P53; 1.
PRINTS; PR00386; P53; 1.
PRODOM; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
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Cellular tumor antigen p53 (Tumor suppressor p53)
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                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 LETRDGOVLGRRCFEARICACPGRDRKADEDSIRKQOVSDSTKNGDGTKRPFRQNTHGIQ 347
        channel catfish (Ictalurus punctatus).";

Comp. Blochem. Physiol. 1208:675-662(1998).

-I-FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinasses. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORILATION (BY SIMILARITY).
1B89CD98DB3289F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
"Identification and characterization of the tumor suppressor p53 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 MTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 399
                                                                                                                                                                                                                                                                                                                                                                             Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Phosphorylation; Apoptosis.

1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 376;
                                                                                                                                  expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 07, Created)
(Rel. 07, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.9%; Score 795;
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                                                                                                                                                                                                                                                                                                              InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                          EMBL; AF074967; AAC26824.1; -. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41989 MW;
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347
286
375
375 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1988
01-APR-1988
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156;
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P07193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 9:109-120(1994).

-! FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94134403; PubMed-8302570;
Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;
"Overexpression of wild-type p53 interferes with normal development in Nenopus laevis embryos";
                                                                                                                                                                                                                                                                                                                                                                                                                                Soussi T., de Fromentel C.C., Mechali M., May P., Kress M.; "Cloning and characterization of a cDNA from Xenopus laevis coding for a protein homologous to human and murine p53."; Oncogene 1:71-78(1987).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Activator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.3%; Score 777.5; DB 1; Length 363; 42.5%; Pred. No. 2.8e-45; Live 55; Mismatches 95; Indels 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CE1F3E58F020D74D CRC64;
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MISSING (IN REF. 2).
MISSING (IN REF. 2).
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OLIGOMERIZATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M36962, AAA49923.1; -. EMBL, X05191; CAA28821.1; -. EBMBL, X77546; CAA54672.1; -. EMBL, S68353; AAC60746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A29376; A29376.
HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
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                                                                                                                                                                          Kenopodinae; Xenopus
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52
71
296
363 AA;
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                          SPPPRGSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYM 181
                                                                                                                                                EDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLG 297
                                                                                                                                                                                                    242 RRCFEVRVCACPGRDRRTEEDDNYTKRGLKPSGK-----RELAHPPSSEPPLPKKR 292
                   58 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF_117
                                                            118 DALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM 177
                                                                                                                                                                                       RRCFEARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKR 354
                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LAADMT
                                           ------AVPTVT-
                                                                                                     178 TPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYV
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes, Tetraodontidae, Tetraodontiformes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TQ THE P53 FAMILY.
SSETGMDPPLSQETFEDLWSLLPDPLQTVTCRLDNLS-EFPDYP--
                                                                                                                                                                                                                                  R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 393
                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                           367 AA
                                       53 VLQE-----GLMGN----
                                                                                                                                                                                                                                                                                                                                                                                  Tetraodon miurus (Congo puffer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF071571; AAD34213.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Ovary;
                                                                                                                                                                                                                                                                                                                                                                       TP53 OR P53
                                                                                                                                                                                                                                                                                                          P53_TETMU
Q9W679;
                                                                                  89
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71 QYTNLGLL-NSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS-----PDDELLY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 GRDRKTEETNSTKMQ-----NDAKDAKKRKSVPTPDSTTIKKSKTASSAEEDNNEVYT 312
                                                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                              41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                   LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                            10 LSQDTFQDLWDNVSAP----PIS----TIQTAALENEAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 AEROMNAMCNFMDSTFNEALFNLLP-------EPPSRDGANSSSPTVPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99422034; PubMed=10490836;
Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
"Nucleotide sequence of the porcine p53 cDNA, and the detection of
recombinant porcine p53 expressed in vitro with a variety of anti-p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Sus.
                                      Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                           DB 1; Length 367;
                                                                                                                                                                                                                                                                                            ; Pred. No. 3.6e-45;
53; Mismatches 105; Indels
                                                                                                                                                                                                                                ACC10EEE2F5F9CFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p
                                                                                                                BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
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313 LQIRGRKRYEMLKKINDGLDLLENKPK 339
                                                                                                                                                                                                                                                                         Score 776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364 LPVRGRETYEMLLKIKESLELMQYLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                           41266 MW;
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                                                                                                                                                                                                                                                                                                                      Matches 165; Conservative
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ProDom; PD002681; P53;
PROSITE; PS00348; P53;
                                                                                                                                                                                                                           367 AA;
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scrofa (Pig).
                                                                                                           86
308
342
288
366
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16-OCT-2001
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                                                                                                           DNA_BIND
DOMAIN
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DOMAIN
MOD_RES
SEQUENCE
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Best Local
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ProDom;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAMP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||:||:||:|||:||| ::::| :|| || ||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VTNWLDENPDDASRVPAP-----PAATAPAPAPAPATSWPL--SSFVPSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 YEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPG
 Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                       NUCLEAR LOCALIZATION SIGNAL (POTÉNTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                   DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 TYEMLLKIKESLELMQYLPQHTIETYRQ--QQQQQHQHLLQKQTSIQSPSSY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                      Anti-oncogene; DNA-binding; Transcription regulation; Activato: Nuclear protein; Phosphorylation; Apoptosis.

1 45 TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                             BASIC (REPRESSION OF DNA-BINDING)
           FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                           68; Mismatches 124; Indels
                               SUBUNIT: Binds DNA as a homotetramer (By similarity). SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                 A4C3D88E8DF55162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       28.0%; Score 771; DB 1; 40.3%; Pred. No. 8.3e-45;
                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 AA.
                                                                                     SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
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                                                                                                                                                                                                                Interpro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SQPPRESSR.
PRODOM; P0002681; P53; 2.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                            EMBL; AF098067; AAF04620.1; -. HSSP; P04637; 1C26.
                                                                                                                                                                                                                                                                                                                                                                                  42862 MW;
                                                                           many types of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                           166; Conservative
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                                                                                                                                                                                                                                                                                                       285
349
380
316
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                                                                                                                                                                                                                                                                                                                                                                                 386 AA;
                                                                                                                                                                                                                                                                                                                   318
361
304
                                                                                                                                                                                                                                                                                                      DNA_BIND
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                             DOMAIN
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ID P53_F
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Vet. Med. Sci. 55:801-805(1993).

J. Vet. Med. Sci. 55:801-805(1993).

-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
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PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBGNIT: Binds DNA as a homotetramer (By similarity).
-:- SUBCELLULAR LOCATION: Nuclear.
-:- DISRARE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
-:- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                              Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okuda M., Umeda A., Sakal T., Ohashi T., Momoi Y., Youn H.Y., Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.; "Cloning of felline p53 tumor-suppressor gene and its aberration hematopoietic tumors."; Int. J. Cancer 58:602-607(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Goitsuka O'Brien S.J., Tsujimoto H., Hasegawa A.; "Molecular cloning and chromosomal mapping of feline p53 tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY SIMILARITY)
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R (IN REF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94114699; PubMed=8286534;
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Lymph node;
MEDLINE=94333960; PubMed=8056458;
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 34-354 FROM N.A.
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Pfam; PF00870; P53; 1.
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386 AA;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      suppressor gene.";
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression.
                                                                                                                                                    IP53 OR TRP53
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Length 386;

DB 1;

Score 770;

28.0%;

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an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                    308
347
292
366
367 #
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                                                                                                                                                             DOMAIN
DNA_BIND
DOMAIN
                                                                                                                                                                                                                                           SEQUENCE
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Best Local
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MOD_RES
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               7
                                                                                                                                            127 ----PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ 182
                                                                                                                                                               SFVPSQKTYPGAYGFHLGFLQSGTAKSVTCTYSPPLNKLFCQLAKTCPVQLWVRSPPPP 145
                                                                                                                                                                                                                                                      243 GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE 302
                                                                                                                                                                                                                                                                                                            303 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELL 362
                                                                                          71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAI---- 126
                                                                                                                                                                                                   GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT 242
                                                                                                                                                                                                                265 VRVCACPGRDRRTEEENFRKKGEPCPEPPGSTKRALPPST---SSTPPOKKKPLDGEYF 321
                                                                  48
                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 16:11383-11383(1988).

-I-FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                      11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                      -----VANWLDEA-----PDDASGMSAVPAPAAPAT----PAPAISWPL
                                                               14 LSQETFSELWNLLPE------NNVLSSELSSAMNELPLSED------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
               60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression (By similarity).
-- SUBCHILLIA BINGS DNA as a homotetramer (By similarity).
-- SUBCELLUIAN LOCATION: Nuclear.
-- SIMILARITY: BELONGS TO THE P53 FAMILY.
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Tumor suppressor p53)
ed. No. 9.7e-45;
Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor i
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 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SPAFAS;
MEDLINE=89083584; PubMed=3060861;
            58;
              161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gallus (Chicken).
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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P10360;
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 Best Local
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Gallus
              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 GRDRKADEDSIRKQQVSDSTKNGDG - TKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LEPTEVFMDLWSMLPY---SMQQL-----PLPEDHSNWQELS----PLEPSDPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 PPPLPL----TPPRAAPSPVVPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                               BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
PRO3TOOFCDF9195B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Leukocyte;
MEDLINE=98178659; PubMed=9519881;
Veldhor N., Milner J.;
"Isolation of canine p53 cDNA and detailed characterization of the full length canine p53 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Canis.
                                                                                                                                                                                                                      Transcription regulation; Activator;
                                                                                                                                                                                                                                    Nuclear protein, Phosphorylation, Apoptosis.
DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 2.1e-44;
50; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
n p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 764.5; DB 1;
Pred. No. 2.1e-44;
                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRETYEMLLKIKESLELMQ 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 GRRYEMLKEINEALQLAE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P53_CANFA STANDARD; F Q29537; Q9TV78; O1-NOV-1997 (Rel. 35, Created) 15-DEC-1998 (Rel. 37, Last sequence 1998 (Rel. 41, Last anno 28-FEB-2003 (Rel. 41, Last anno 28-FEB-2003 (Rel. 41, Last anno 29-FEB-2003 (Rel. 41) (Rel. 41)
                                                                                                     Pram; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDon; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                      40169 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular tumor antigen p53 TP53 OR P53.
EMBL; X13057; CAA31456.1;
PIR; S02193; S02193.
HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                        339
364
306
366
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--ATSAPTAPGP--APSWPL----SSSVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97305153; PubMed-9161419;
                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 189:101-106(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Himedaka;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8090;
  64 P----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exposed fish.
                                                                                                                                                                                                                                                                                                         ORYLA
                                                                                                                                                                       310
                                                                                                                                                                                                                     370
                                                                                                                                               207
                                                                                                                                                                                             267
                                                                                                                                                                                                                                             324
                                                                                                                                                                                                                                                                                           P53_ORYLA
ID P53_C
                                                                                                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
A., Tsujimoto H.;
                                                                                                                                                    LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSD-PMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY PRPK) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>-</del>-
                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety of transformed cells, p53 is frequently mutated or inactivated
                                                          Matari T., Hasagawa A., Tsujimoto H.;
Aberrations of p53 tumor suppressor gene in various spontaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASIC (REPRESSION OF DNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY).
MEES -> MQEP (IN REF. 2).
                                                                                                                                                                                                                                                                                                     SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                               Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                761A718FDC93DA59 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.6%; Score 758.5; 39.3%; Pred. No. 5.6
                                                                                                                                             MEDLINE-95323915; PubMed-7600529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF060514; AAC16909.1; --
EMBL, AAD20761; BAA78379.1; --
EMBL, S77819; AAB42022.1; --
HSSP; P04637; IOLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00870; P53; 1.
PRINTS, PR00386; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42486 MW;
 Oncogene 16:1077-1084(1998).
                                                                                                                      SEQUENCE OF 25-300 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       many types of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                               Setoguchi A., Sakai T.,
Watari T., Hasagawa A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                      SEQUENCE FROM N.A.
                                                                                   dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313
356
299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380
                                 TISSUE-Spleen;
                                                                                   tumors in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
DOMAIN
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Matches
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                                                                                               249
189
                                                                                                                        PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIIVTLETRDGQVLGRRCFEARICACP 309
                                                                                                                                                                                                                          |||||: :|:: |: | : | :||| :| :||| GRDRRTEEENFHKKGEPCPEPPPGSTKRALPPST---SSSPPQKKKPLDGEYFTLQIRGR 323
                                                88 KTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCOLAKTCPVOLWVSSPPPPNTCVRAM 147
                                                                                                                                                                                                                                                                                               GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 369
                                                                                                                                                                                                                                                                                                                                                                                            ETYEMLLKIKESLELMQYLP-----QHT--IETYRQQQQQQQQHLLQKQTSIQS 416
                                                                                                                                                                                                                                                                                                                                                                                                                           130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;

"Isolation of CDNAs encoding the p53 tumor suppressor gene in the
"Isolation of CDNAs encoding the p53 tumor suppressor gene in the
Japanese Medaka (Oryzias latipes).";

Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes regulated for this process. One of
the activated genes is an inhibitor of cyclin dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Japanese medaka
hotspots in MNNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
SUBGNIT: Binds DNA as a hootetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                797820; OGPSU7; OGPSU8; 01-NOV-1997 (Rel. 35, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryzias latipes (Medaka fish) (Japanese ricefish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krause M.K., Rhodes L.D., van Beneden R.J.; "Cloning of the p53 tumor suppressor gene from (Oryzias latipés) and evaluation of mutational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352
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us-09-538-106-14.rsp

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                                                                                                                                                                                                                                                                                                                                                                    EHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQ 255
                                                                                                                                                                                                                                                                                                                                                                                                         256 VGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPGRDRKA 315
                                                                                                                                                                                                                                                                                                                                                                                                                   76 GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGP 135
                                                                                                                                                                                                                                                                                                                                 136 HSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAMPVYKKA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                   14 FQELWETVSYP--PLETLSLPTVNEPTGSW-----VATGDMFLLDQDLS------55
                                                                                                                                                                                                                                                                                                               91
                                                                                                                                                                                                                                                                                                                                            ||| :||:||:||:||
EHVADVVRRCPHHQ-----NEDSVEHRSHLIRVEGSQLAQYFEDPYTKRQSVTVPYEPPQ
                                                                                                                             BY SIMILARITY.
OLIGOMERIZARION
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                       FQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQYTNL
                                                                                                                                                                                                                                                                                                              DEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS------PDDELLYLPVRG
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine), and Bos indus (Bovine).
Bos indiaus (2001).
Eukaryola: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                            HSSP; P04637; 1YCS.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P538UPPRESSR.
ProDom; PD00268; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                            Nuclear protein; Phosphorjiation; Apoptosis; Polymorphism.

DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                   DB 1; Length 352;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                        ISSING (IN REF. 1).
196868A66351BFF5 CRC64;
                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
TP53.
                                                                                                                                                                                                                  27.1%; Score 746.5; DB 1
43.1%; Pred. No. 3.3e-43;
tive 54; Mismatches 92
                                                                                                                                                                              S -> T.
MISSING (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 AA.
or send an email to license@isb-sib.ch)
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RERYEFLKKINDGLELLE 329
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                EMBL; U57306; AAC60146.1; -.
EMBL; AF003949; AAD01195.1; -.
EMBL; AF003950; AAD01196.1; -.
                                                                                                                                                                                                39753 MW;
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                               273
331
350
295
351
91
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NCBL_TaxID=9913, 9915;
                                                                                                                                                                                              352 AA;
                                                                                                                                                                                                                            Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P53_BOVIN
Q29628;
                                                                                                                              DOMAIN
DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
                                                                                                                                                                                                                                                                                                                                                                                      152
                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                     MOD_RES
                                                                                                                                                                                        CONFLICT
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Matches
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P53_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 SPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTEL
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                                                                                                                                                                        Comori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.; "Predominant p53 mutations in enzootic bovine leukemic cell lines."; Vet. Immunol. Immunopathol: 52:53-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
-1- SUBCELDULAR LOCATION: Nuclear.
-1- DISBASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
             Dequiedt F., Kettmann R., Burny A., Willems L.;
"Nucleotide sequence of the bovine P53 tumor-suppressor CDNA.";
DNA Seq. 5:261-264(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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NUCLEAR LOCALIZATION SIGNAL (POTE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in many types of cancer.
-- SIMILARITY: BELONGS TO THE P53 FAMILY.
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222473F28C548F31 CRC64;
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SEQUENCE OF 13-386 FROM N.A.
SEQUENCE SEOURINE: STRAIN-HOLStein; TISSUE-Thymus;
MEDLINE-96401400; PubMed-8807776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.9%; Score 740; DB 1, 45.8%; Pred. No. 1e-42; iive 57; Mismatches
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OLIGOMERIZATION
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MEDLINE-95352829; PubMed-7626789;
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EMBL; D49825; BAA08629.1; -.
EMBL; U74486; AAB51214.1; -.
PIR; S51648; S51648.
HSSP; P04637; ITUP.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPRESSR.
ProDom; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
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380
386 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIANE—9737696; PubMed=9233767;

MEDIANE—9737696; PubMed=9233767;

MEDIANE—9737696; PubMed=9233767;

Rettelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.W.;

Rettelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.W.;

The perfect characterization of the woodchuck tumor suppressor, p53, and its interaction with woodchuck hepatitis virus X antigen in The perfect characters of the woodchuck tumor suppressor, p53, and growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.

Apoptosis induction seems to be mediated either by stimulation of mannear and PAS antigen expression, or by repression of BCI-2
RPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPF 339
                                                                                                                                                                                                     RONTHGIQMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQ 398
                                                                     APPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear. DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                399 QQQQQH-QHLLQKQTSIQSPSSYGNSSPPLNK 429
                                                                                                                                                                                                                                                                                 353 GESRAHSSHLKSK----KRPSPSCHKKPMLKR 380
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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HSSP; P04637; 1TUP.
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Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marmota monax (Woodchuck)
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                           LSQETFSDLWNLLP-----ENNVLSPVLSP 38
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                                                                                                                                                                                                                                                                                                     11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                               71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA----
                                                                                                                                                                                                                                                                                                                                                                                                                     39 PMDDL-LLSSED--VENWFDK----GPDEALQMSAAPAPKAPTPAASTLAAPSPATSWPL
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                                                                                                           NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                   78; Gaps
Transcription regulation; Activator;
           phosphorylation, Apoptosis.
TRANSCRIPTION ACTIVATION (ACIDIC).
                                                   BY SIMILARITY.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE)
                                                                                                                                                                   PHOSPHORYLATION (BY SIMILARITY). E1DE5DB84BA40182 CRC64;
                                                                                                                                                                                                                             Length 391;
                                                                                                                                                                                                                                                                 70; Mismatches 121; Indels
                                                                                                                                                                                                                             DB 1;
1.4e-42;
                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                             26.8%; Score 738; 37.7%; Pred. No. 1
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                                                                                                                                                                                       43468 MW;
DNA-binding;
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                                                     290
354
385
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15
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                   Nuclear protein;
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323
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Anti-oncogene;
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SEQUENCE
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                                                   DNA_BIND
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Matches
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Q991b6 homo sapien O991b6 homo sapien O9939 homo sapien O9930 rattus norv O9074 homo sapien O891b2 brachydanio Q81bz6 brachydanio Q81bz6 brachydanio Q81bz6 brachydanio Q81bz6 brachydanio Q81bz6 brachydanio Q81bz mus musculu Q91bz mus musculu Q81dy6 homo sapien Q84dy6 homo sapien Q8cdy6 mus musculu Q8nhw9 homo sapien Q9cdy7 mus musculu Q8nhw9 homo sapien
                        089097 mus musculu
089097 mus musculu
099162 rattus norv
090132 homo sapien
099191 rattus norv
089190 rattus norv
088897 mus musculu
Q9ubv9 homo sapien
Q9p1b4 homo sapien
O75080 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andraws N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3427-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                               ALIGNMENTS
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        09P1B4
075080
099U62
099U62
099JB2
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099JB6
099JB6
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099JD9
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Q8TDY5
Q8C826
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Q8JHZ5
Q8JHZ6
Q8B899
Q98SW0
Q9W664
Q9JJP2
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Q9CU77
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                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2002 (TrEMBLrel. 22, P63.
                                                                                             AAC62637.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
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09н3D3;
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EMBL;
EMBL;
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HSSP;
 09h3d3 homo sapien
09plb7 homo sapien
095195 homo sapien
099jd7 rattus norv
099jd8 rattus norv
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homo sapien
homo sapien
9 mus musculu
                                                       August 7, 2003, 09:41:09; Search time 41.5172 Seconds (without alignments) 3207.225 Million cell updates/sec
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Q9up26 hc
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                   of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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2751
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Match Length DB
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Query Match
Best Local Similarity
Matches 515; Conserv
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SEQUENCE FROM N.A.
                 EMBL; AF116761; A
EMBL; AF116762; A
EMBL; AF116763; A
EMBL; AF116764; A
EMBL; AF116765; A
EMBL; AF116766; A
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SEQUENCE 516
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
P51 isoform Tap63beta.
Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutation and expression of the p51 gene in human lung cancer."; popplasia 1:71-79(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AF116755; AAF43488.1; --
EMBL; AF116755; AAF43488.1; JOINED.
EMBL; AF116757; AAF43488.1; JOINED.
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                                                                          DB 4; Length 555;
                                                                                             Indels
                                                      E22874BE7DBABCBE CRC64;
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Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto
Yokota J.;
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100.0%; Pred. No. 2e-223;
11ve 0; Mismatches 0;
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      Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53sUPPRESSR.
ProDom; P0002681; P53; 1.
PROSITE; P500348; P53; 1.
                                             Nuclear protein.
SEQUENCE 555 AA; 62433 MW;
InterPro; IPR002117; P53.
                                                                                 Best Local Similarity 100.
Matches 516; Conservative
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                                                                                                                                                                                                                                                                                                                                                          1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                         Length 516;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
P51 isoform TAE63ALPHA (P51B protein).
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                                                                                                                                                                                                                                                                                       99.7%; Score 2744; DB 4;
99.8%; Pred. No. 7.2e-223;
Live 0; Mismatches 1;
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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AAF43488.1;
AAF43488.1;
AAF43488.1;
AAF43488.1;
AAF43488.1;
AAF43488.1;
AAF43488.1;
                                                                                                                     AF116767; AAF43488.1;
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                                                                                                                                                       InterPro; IPR002117; P53
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421 GNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGL
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MEDIATE=98448055; WEAR 480055; M. Gillett E., Fleming M.D., Dotsch V.,
Xang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
Andrews N.C., Shomolog at 3427-29, encodes multiple products with
Transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                             Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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A Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
REMBL; AF124529; AAG45607.1; JOINED.
REMBL; AF124531; AAG45607.1; JOINED.
REMBL; AF124531; AAG45607.1; JOINED.
REMBL; AF124533; AAG45607.1; JOINED.
REMBL; AF124533; AAG45607.1; JOINED.
REMBL; AF124535; AAG45607.1; JOINED.
REMBL; AF124535; AAG45607.1; JOINED.
REMBL; AF124535; AAG45607.1; JOINED.
REMBL; AF124536; AAG45607.1; JOINED.
REMBL; AF124537; AAG45607.1; JOINED.
REMBL; AF124538; AAG45607.1; JOINED.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                          Q9H3D4; Q9UP28; 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
TA p63 alpha (Tumor protein p63).
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100.0%; Pred. No. 7.5e-221;
ive 0; Mismatches 0;
                                                                                            481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
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nes 511; Conservative
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              MEDLINE-98324755; Pubbwed-9662378; Osada M., Obba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I., Ikawa Y., Nimura Y., Nakagawara A., Obinata M.; "Cloning and functional analysis of human p51, which structurally a functionally resembles p53."; Nat. Med. 4:839-844(1998).
                                                                                                                                                                                                                                                                        "Mutation and expression of the p51 gene in human lung cancer."; Neoplasia 1:71-79(1999).
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Yokota J.;
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                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AB016073; BAA32593.1; -.
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MEDLINE-20388515; PubMed-10935472;
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PRINTS; PR00386; P53SUPPRESSR.
PRINTS: PD002681; P53; 1.
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Interpro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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Matches 511; Conservative
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TISSUE-Skeletal muscle;
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SEQUENCE 641 A
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                                                                    SPSPAIPSNIDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                              203 PQGAVIRAMPVXKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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MSQSTQTSEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSENGATNKIEISMDCIRMQ
                                   PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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MEDLINE-21363378; PubMed=11470269;
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PRINTS; PR00386; P53SUPPRESSR.
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Best Local Similarity 98.4%;
Matches 508; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE 555 #
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01-OCT-2002
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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Last sequence update)
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Pred. No. 2.6e-220;
5; Mismatches 3;
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FEBS Lett. 501:121-126(2001).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIM)
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
BEBLE, AD277452; ACC37104.1; -.
HSSP; P04637; 1YCS.
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MEDLINE=21363378; PubMed=11470269;
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PRINTS; PR00386; P535UPPRESSR.
ProDom; PD002081; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 538 AA; 60326 MW;
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                variants...;
FEBS Lett. 501:121-126(2001).
-i SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; A277451; CAC37103.1; -.
HSSP; P04637; 1YCS.
InterPro; IPR002117; P53.
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Pred. No. 2.7e-220;
5; Mismatches 3;
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TISSUE—Skeletal muscle, and Keratinocytes;

MEDLINE—9901825; Pubmed—979841;

Augustin M., Bamberger C., Paul D., Schmale H.;

"Cloning and chromosomal mapping of the human p53-related KET gene to chromosome 3427 and its muthe homolog Ket to mouse chromosome 16.";

Mamm. Genome 9:899-902(1998).

-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-! STHILARITY: BELONGS TO THE P53 FAMILY.

EMBL; Y16961; CAA76562.1;

HSSP; P04637; 1YCS.
                                                                                                                                                SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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              MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last annotation update)
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ProDom; PD002681; P53; 1.
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InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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PROSITE; PS00348; P53; 1.
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                                                     SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
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                                       DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
SPSPAIPSNIDYPGPHSFDVSFQQSSTAKSATWIYSTELKKLYCQIAKTCPIQIKVWIPP
                                                                                                                                                          MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.
Caput D., McKeon F.;
Pp63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
MOI. Cell 2:305-316(1998).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV 516
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HSSP; P04637; 1YCS.
MGD; MGI:1330810; Trp63.
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Pfam; PF00870; P53; 1.
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SEQUENCE 555
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rat
NCBL_TaxID=10116;
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                                                    Length
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL: Y10258; CAB88216.1; -.
HSSP; P04637; IXCS.
                  C953BBAC389D5B70 CRC64;
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Last annotation update)
                                                    DB 11;
                                                  Score 2685; DB 11;
Pred. No. 9.6e-218;
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MEDLINE-97460723; PubMed-9315105;
                                                                                     5,
                  74660 MW;
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                                                 97.6%;
illarity 98.4%;
Conservative
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Best Local Simi
Matches 503;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDILINE-21363781, PubMed=11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution of novel KET/p63 splice
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Length 680;
                                  Indels
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Score 2714; DB 4;
Pred. No. 3.6e-220;
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98.7%;
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THE P53 FAMILY
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InterPro; IRR002117; P53.
InterPro; IRR001660; SAM.
Pfam: PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
                      EMBL; AF075436; AAC62641.1;
HSSP; P04637; 1YCS.
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Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Murinae; Mus
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                                                                                                                                                                                                  DB 11; Length 680;
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                                                                                                                                                              AC45DABB88F61400 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCBI_TaxID=10090;
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Last annotation update)
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-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                              Score 2685; DB 11;
Pred. No. 1e-217;
5; Mismatches 3;
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InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P533UPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                         680 AA; 76760 MW;
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22,
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Best Local Similarity 98.4
Matches 503; Conservative
                                                                                                                  PROSITE; PS00348; P53; 1.
Nuclear protein.
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                                                                                                                           40 MSQSTQTSEFLSPEVFQHIMDFLEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQ
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                                                                                                          1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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MEDLINE-20388515; PubMed-10935472;
MIDLINE-20388515; PubMed-10935472;
Yound M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S., Yokota J.;
Mutation and expression of the p51 gene in human lung cancer.";
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                                    680;
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
NCBI_TaxID=9606;
                                    DB 11; Length
                                                                      Indels
 8DFF0284F247C68A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
P51 isoform Tap63delta (P51 delta protein).
                                97.6%; Score 2685; DB 11;
98.4%; Pred. No. 1e-217;
1ve 6; Mismatches 2;
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680 AA; 76788 MW;
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70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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                                               MEDLINE-98448095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3427-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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                                                                                                                                                                                                                                                                                     461 AA; 51404 MW; 68B63547A46C1B05 CRC64;
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ProDom; PD002681; P53; 1.
PROSTTE; PS03348; P53; 1.
Nuclear protein.
SEQUENCE 461 AA; 51404 MW;
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Pfam; PF00870; P53; 1.
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Matches 447; Conservative
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 471;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 AA; 52882 MW; 32EB39798FC1CE69 CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2449; DB 4; I; Pred. No. 4.8e-198;
                      - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
- SIMILARITY: BELONGS TO THE P53 FAMILY.
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                                                                                                EMBL, AFIL6769, ARF4348911; EMBL, AFIL6755, ARF4348911; JOINED. EMBL, AFIL6759; ARF4348911; JOINED. EMBL, AFIL6759; ARF4348911; JOINED. EMBL, AFIL6760; AAF4348911; JOINED. EMBL, AFIL6761, ARF4348911; JOINED. EMBL, AFIL6762; AAF4348911; JOINED. EMBL, AFIL6765; AAF4348911; JOINED. EMBL, AFIL6766; AAF4348911; AAF4348911
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Matches 463; Conservative
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Neoplasia 1:71-79(1999)
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SEQUENCE 471 P
                                                                          EMBL; AF116771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AC Q9UP26;
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                                                                                                                                           01-MAY-2000
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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| Neoplasia 1:71-79(1999).
| Rembl. API16769; AAF43492.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                               P51 isoform delMbeta.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE-20388515; Pubmed-10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2372; DB 4; Length 461;
Pred. No. 1.5e-191;
0; Mismatches 1; Indels
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                                    (TrEMBLrel. 15, C (TrEMBLrel. 15, I (TrEMBLrel. 22, I
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99.8%;
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hes 446; Conservative
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  PRELIMINARY
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Nuclear protein.
SEQUENCE 461 P
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01-OCT-2000 (
01-OCT-2002 (
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                                                                                                                                                                                                                                                                MEDLINE-98448095; PubMed-9774969; Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.; Po63, a p53 homolog at 3q27-29, encodes multiple products with ransactivating, death-inducing, and dominant-negative activities."; Mol. Cell 2:305-316(1998).

-i - SubCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i - SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL: AF075438; AAC62643.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 PQYTNLGLINSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 AA; 51455 MW; 7613296F2F85DBC8 CRC64;
                                    (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.6%; Score 2356; DB 11;
98.9%; Pred. No. 3.2e-190;
tive 3; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCD: MCI:1330810; Trp63.
InterPro; IPR002117; P53.
Fram; PF00840; P53; L.
PRINTS; PR00386; P53; L.
PRODOM; PD002681; P53; L.
Nuclear profein.
SEQUENCE 461 AA; 51455 MW; 7
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Search completed: August 7, 2003, 09:51:38 Job time : 42.5172 secs

Human oncogene p51 Human oncogene p51

Human p63 protein
Human nccogene p63
Human nccogene p63
Human lung cancer
Human p51 protein
Human p51 protein
Human p63 protein
Human p63 protein
Human nccogene p58
Human nccogene p61
Human nccogene p63
Human nccogene p61
Human nccogene p61
Human p63 protein

Rat KET protein.
Human cell regulat
Human oncogene p51
Human oncogene p63
Mouse cell regulat

Human oncogene p51 Human p63 protein oncogene p51

lung cancer p53 homologu cell regulat

Human Human Human Human Human

Run on:

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ABG95141
ABP61915
ABB74995
                             AAY45247
AAY05953
AAB11358
AAB82129
ABG95128
ABG95136
                                               ABG95142
ABP61910
ABB74990
AAB11361
                                                                                ABG95139
AAY05964
ABG95130
                                                                                                ABG95138
ABP61914
ABB74994
AAY05956
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ABB74993
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August 7, 2003, 09:31:28; Search time 30.8966 Seconds (without alignments) 2301.535 Million cell updates/sec
                                                                                        2383
1 MSGSTQTNEFLSPEVFQHIW......PKQSDVFFRHSKPPNRSVYP 448
  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                          Total number of hits satisfying chosen parameters:
                                                     1107863 seqs, 158726573 residues
                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
              OM protein - protein search, using sw model
                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
                                US-09-538-106-15
                                                                                                                    Minimum DB seq
Maximum DB seq
                                Title:
Perfect score:
                                            Scoring table:
                                                     Searched:
                                      Sednence:
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human p51 protein	Human cell requlat	Human p63 protein	Human protein #1 u	Human oncodene p51	Human oncodene p51	Human oncodene p63	Human lung cancer	Human p53 homologu
SUMMARIES		AAY05955	AAB11359	AAB82128	ABG95127	ABG95137	ABG95143	ABP61911	ABB74991
DB	20	20	21	22	23	23	23	23	23
% Query e Match Length DB	448	448	448	448	448	448	448	448	448
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	2383	2383	2383	2383	2383	2383	2383	2383	2383
Result No.		7	m	4	S	9	7	80	σ

		ALIGNMENTS
RESU AAY4	RESULT 1 AAY45246	
Π	AAY45246 standal	AAY45246 standard; Protein; 448 AA.
XX		
X X	AAY45246;	
DŢ	07-JAN-2000 (first entry)	irst entry)
X E	Human n51 protein A	est control of the co
×		
KW	Human; p51; p53	Human; p51; p53 related gene; cell proliferation; requlation; cancer;
KW	tumour suppress.	suppression; diagnosis.
YY	1	
S ×	HOMO Sapiens.	
1 1 1		Togation (One) if fiore
4 6	Domain	LOCALIDITY QUALITIES
FL	***************************************	/label= transactivation domain
F	Domain	142 321
FT		/label DNA binding domain
FT	Domain	353397
FT		/label= oligomerisation_domain
N N	W09950412-A1.	
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PD	07-OCT-1999.	
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PF	24-MAR-1999;	99WO-JP01512.
PR	27-MAR-1998;	98JP-0100467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE 420
                                                                                                                                                                                                                                                                 The present sequence represents a human p51 protein, which is related to p53 and has cell proliferation requiation and tumour suppression activity. The p51 gene can be used in the investigation, diagnosis and treatment of diseases such as cancer, with which the p53 family cell proliferation regulation is associated. The p51 protein may be used for screening potential agonists and antagonists of its regulatory function, for use as drugs,
                                                                                                                                                                                                                                                        1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGAINKIEISMDCIRMQ 60
                                                                New p53 related human gene p51, useful for diagnosis, investigation and treatment of cancers and screening for potential cell proliferation
                                                                                                                                                                                                                                                                                                                                          PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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                                                                                                                                                                                                                      Length 448;
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                                                                                                                                                                                                                   33; DB 20;
4.7e-207;
                                                                                                                                                                                                                  100.0%; Score 2383;
100.0%; Pred. No. 4.7
:ive 0; Mismatches
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                                                                                                       Claim 1; Page 147-148; 163pp; Japanese.
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                  Obinata M;
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                                                                                                                                                                                                                                     Matches 448; Conservative
                                    WPI; 1999-591318/50
                  Ikawa S,
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                                                                                                                                                                                                  448 AA;
                                              N-PSDB; AAZ25770
(IKAW/) IKAWA Y.
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                  Ikawa Y,
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The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron is conserved between p73 and p53, and from known exon and intron is conserved domain and their intervening identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position and intron. The human p53 gene was localised to chromosomal position affering at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as delian and A forms, where the deltan form lacks the transactivation domain. The present sequence represents human p63 isotype TAp63 gamma. D63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous and p63, and as a critical role in the process of cervical squamous proposed in the process of cervical squamous process of p63 may also be implicated in haematopolasis, muscle wasting (e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated p63 cell regulatory protein for, e.g. treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 23; Fig 11; 161pp; English.
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Matches 448; Conservative
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Homo sapiens.
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Score 2383; DB 21;
Pred. No. 4.7e-207;
Mismatches 0;
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/label= DNA_binding_domain
353..397
/label= Oligomerisation_domain
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N-PSDB; AAF86588.
                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300 HIHIHIHIHIHIHIHIHIHIHIH 300 241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300
                                                                                                      comprising an immunogenic parties of a lung purported of a minimum which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting development of cancer.
 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
                                                                                        FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
                                                                                                                                                 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQOHQHLLQKHLLSACFRNE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel isolated polypeptide (I) which
                                                                                                                                                                                                                            LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 247-249; 261pp; English.
                                                                                                                                                                                                                                                                                                               AAB11359 standard; Protein; 448 AA
                                                                                                                                                                                                                                                                                                                                                                                                        Human p63 protein isoform #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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N-PSDB; AAC66029.
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30-DEC-1999;
10-JAN-2000;
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AAB11359
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WO200269900-A2.
Chimera gene of the p53 family, useful for gene therapy, and treatment of cancer, comprises a transcription activating region and a DNA
                                                                                                                                                       Example 1; Page 30-32; 57pp; Japanese
                                                                                  binding region
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The present invention relates to a chimera gene of p53 family encoding a transcription activating region, a DNA binding region, and an oligomer formation region of different p53 family proteins. The chimeric gene can be used for gene therapy of p53 variant human tumours, and analysis of the function of the p53 family gene. The present sequence was used in the present invention.

448 AA; Sequence

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                                                                                        ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 300
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                                                 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                      1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                              DSDLSDPMWPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                    SPSPAIPSNIDYPGPHSFDVSFQQSSTAKSATWIYSTELKKLYCQIAKTCPIQIKVMIPP
                                                                                                                                                          PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                                                           LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE
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   Length 448;
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  100.0%; Score 2383; DB 22; 100.0%; Pred. No. 4.7e-207;
                    Mismatches
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Ź ABG95127 standard; Protein; 448 (first entry) Human oncogene p51A. 04-DEC-2002 ABG95127; RESULT 5

180 180 240 240 300 300 360

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> prollferative disease; cellular protein isoform; heat shock protein 90; HSP-90; rheumatoid arthritis; cancer; heamatopoitetic disorder; T cell lymphona; B cell lymphona; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML; papillary thyroblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Eving's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection Chromosome aberration; oncogenic fusion protein; cancer;

Homo sapiens

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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein disease with chromosomal aberration yielding involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cells containing fusion protein in heterogeneous call population, treating proliferative disease (e.g. rheumatoid arthritisty cancer) associated with mutant protein or cellular protein isoform dispendent on heat shock protein or cellular protein isoform dispendent on heat shock protein or cellular protein in a patient heterozygous for (II). The method is useful for treating a disease e.g. hemantopoletic disorder such as T or B cell ymphoma, chronic myeloid leukaemia (CML), APL, AML, MLL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
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                                                                                                                                                                                                                                                                                 (CONF-) CONFORMA THERAPEUTICS CORP
                                                                                                                                      01-MAR-2002; 2002WO-US06518
                                                                                                                                                                                                              01-MAR-2001; 2001US-272751P
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (1), treating cancerous cells containing (1) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (11) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (11) in administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with horromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion concepenic fusion protein, treating cancerous cells containing fusion or cancer associated with mutant protein or cellular protein la spetient heterograpus for (II). The method is useful contein isoform dependent on heat shock protein (HSP)-90 (e.g. postein isoform dependent on heat shock protein or cellular protein and patient heteroxygous for (II). The method is useful for treating a disease e.g. hhematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, AML, AML, NHL and CMML, arrithman and selectively a solid tumour such as papillary thyroid
                         LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabòomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein 90;
                                                                                                                                                                                                                                                                                                                                                                                                            Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 90 proliferative disease; cellular protein isoform; heat shock protein 90 HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; r cell lymphona; B cell lymphona; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML; acute lymphoblastic leukaemia; ALL; APL; NII; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                        421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
                                                                                    LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
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                                                                                                                                                                                                                                                                                                                                                                          Human oncogene p51 isoform TAp63gamma.
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                                                                                                                      61 DSDLSDPWWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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                                                                                                                                                                                                                              LLYLPVRGRETY EMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE
                                                                     1 MSQSTQTNEFLSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIELSMDCIRMQ
                                                                                                                                                                                                                PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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                                                     1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMO
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                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CMI acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia;
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    Length 448;
  23;
             4.7e-207
    DB
100.0%; Score 2383;
100.0%; Pred. No. 4.7
iive 0; Mismatches
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               Best Local Similarity Love. Matches 448; Conservative
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    Query Match
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N-PSDB; ABS73335

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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (MSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for [II]. The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leuksemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarrooma, melanoma, liposarrooma, rhabdomyosarrooma and synovial sarrooma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                      Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                               Disclosure; Page 354-356; 389pp; English
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448 AA; Sequence

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                                      DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                        SPSPAIPSNIDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
                                                                                                                                                                 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                                                                                                                            LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQHQHLLQKHLLSACFRNE
                     Gaps
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   Length 448;
100.0%; Score 2383; DB 23; Length
100.0%; Pred. No. 4.7e-207;
ive 0; Mismatches 0; Indels
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Query Match 100.
Best Local Similarity 100.
Matches 448; Conservative
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standard; Protein; 448 AA.

ABP61911;

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ABP61911

RESULT 8 ABP6191

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polynucleotides (T) and polypeptides (TI) and (TI) have extostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (T) or (TI) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (T) can be used for detecting the presence of a cancer in a patient, by obtaining a bloiogical sample from the patient, contexting the biological sample from the patient, contexting the sample with the Oligonucleotide, detecting in the sample, amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermine of underly and (TI) are useful in paramaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer.

ARQ02145 to ARQ02486 and ABR01866 to ABR01922 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                      Vedvick TS;
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                                                                                 Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes isolated human lung carcinoma
                                                 Human lung cancer associated protein sequence SEQ ID NO:340.
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Durham M, Fanger GR,
W, Cai F, Foy TM;
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4.7e-207;
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100.0%; Pred. No. 4.7
:ive 0; Mismatches
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Retter MW, Di
Peckham DW,
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07-MAY-2001; 2001US-0850716.
28-JUN-2001; 2001US-0897778.
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               (first entry)
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Best Local Similarity 100.
Matches 448; Conservative
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Watanabe Y,
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                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
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                                                                                                                   Homo sapiens.
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McNeill PD,
               07-0CT-2002
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2001US-290492P.
2001US-339245P.
2001US-350666P.
2001US-334370P.
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             448; Conservative
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N-PSDB; ABX76134.
  Best Local Similarity
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10-MAY-2001; 2
09-NOV-2001; 2
13-NOV-2001; 2
29-NOV-2001; 2
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               ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC 300
                                                FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
                                                                                             LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynuclectides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABIA8959 to ABI49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                           Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RA;
                                                                                                                                                                                                                                                                                                  Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD,
McNeill PD, Fanger N, Retter MW, Marnerakis M,
Vedvick TS, Carter D, Watanabe Y, Peckham DW;
                                                                                                                                          LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 2383;
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                                                                                                                                                                                                                          ABB74991 standard; Protein; 448
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2000US-0735705.
2001US-0850716.
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2000US-0643597.
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                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                       immune response.
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09-OCT-2000;
12-DEC-2000;
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21-AUG-2000;
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McNeill
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80% identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polyneptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides of pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides creening for therapeutic compounds that modulate lung cancer, such as attended so a stargets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer, such as
                             Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                                                        Claim 27; Page 196; 453pp; English.
                                                                                                                                expression in lung cancer
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100.0%; Score 2383; DB 24; Length 448; 100.0%; Pred. No. 4.7e-207; ive 0; Mismatches 0; Indels 0; 448; Conservative Local Similarity 448 AA; Sequence Query Match Matches Best

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Gaps

DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120 9 9 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGAINKIEISMDCIRMQ 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 61 61 g à ð Db

SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180 240 SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 121 181 · 영 g ò

121

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ITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC 241 181

> δ a ð g ò a ŏ

FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360

301

transgenic animals.

AAY05961 standard; Protein; 483 AA. AAY05961; RESULT 11 **AA**Y05961

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using RACE. Sequencing of the amplification product indicated that the amplified cDNA possessed a truncated N-terminus, i.e. the transactivation domain was absent. Additional splice variants were identified by screening a cDNA library with a probe corresponding to exons 5-9 of p63. At least 6 different isotypes exist. Splice variants differing at the C-terminus are designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents murine b53 isotype murap63 gamma. D63 was detected in a variety of channan and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate b53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression cityities both benign and neoplastic. DeltaN isotopes of p63 expression act as dominant inegatives towards transactivation by p53 and p63. Cechexia) and neuronal differentiation and neoplastic act as dominant inegatives towards transactivation by p53 and p63. Cechexia) and neuronal differentiation and neoplastic and related degenerative considered and related degenerative considered and related degenerative considered and related degeneration or dechexia) and neuronal differentiation and neoplastic and related degenerative considered and rel disorders, p63 polypeptides (see AAY05953-64), polynucleotides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of mouse; New isolated p63 cell regulatory protein for, e.g. treatment of Cell regulatory protein; p63; muTAp63 gamma; TAp63 gamma; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy. Mouse cell regulatory protein p63, isoform muTAp63 gamma Claim 23; Fig 17; 161pp; English. 98US-0087216. 97US-0062076. 98WO-US21992 16-AUG-1999 (first entry) (HARD) HARVARD COLLEGE. WPI; 1999-277595/23. McKeon F, Yang A; N-PSDB; AAX58580 W09919357-A2 02-OCT-1998; 29-MAY-1998; 15-OCT-1997; 22-APR-1999 Mus sp. tumours

Τ; 61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120 9 66 40 MSQSTQTSEFLSPEVFQHIMDFLEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQ 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ Gaps 4; Length 483; Indels 96.3%; Score 2296; DB 20; 96.9%; Pred. No. 4e-199; ive 3; Mismatches 7; 434; Conservative Query Match Best Local Similarity Matches 434; Conserv 483 AA; Sequence ò g δy g

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420
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 SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 90; HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; cell lymphona; Beell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; ALL; APL; NHL; solid tumour; chronic myeloid leukaemia; CML; papillary thyroid carcinoma; Eving's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                SPSPAIPSNIDYPGPHSFDVSFQQSSTAKSATWIYSTELKKLYCQIAKTCPIQIKVMTPP
                                                          PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                                                                         ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC
                                                                                                                                LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQHQHLLQKHLLSACFRNE
                                                                                                                                                                                                                                                  Treating genetically-defined disease associated with chromosomal
                                                                                                                                                                                                                                                                                             LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
                                                                                                                                                                                                                                                                                                            Disclosure; Page 325-327; 389pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                               ABG95129 standard; Protein; 471 AA
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N-PSDB; ABS73329.
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protein (HSP)-90, or selectively treating cells expressing (II)

treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein, treating cancerous cells containing fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. potein isoform in a patient heteroxygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Enving's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral ciffections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                             Length 471;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                                                                                                                                                                                                                         Score 2185; DB 23;
Pred. No. 4.4e-189;
3; Mismatches 7;
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94.1%;
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                                                                                                                                                                                                                                                                                                        471 AA;
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (1), treating cancerous cells containing (1) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein isoforms (II) dependent on heat shock protein or selectively treating centeron seeful for treating administering HSSD-14nhibitor. The method is useful for treating genetically defined disease with chromosomal aberration yielding protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein for cellular protein isoform apatient heterozygous for (II). The method is useful protein isoform in a patient heterozygous for (II). The method is useful imphoma, chronic myeloid leukemia (CML), APL, AML, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid surching arcoma, melanoma, Ilposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
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                                                                                                                                                                                                                                                                                                                        Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
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                                                                                                                                                                                                        (CONF-) CONFORMA THERAPEUTICS CORP.
                                                                                                                              01-MAR-2002; 2002WO-US06518.
                                                                                                                                                                    01-MAR-2001; 2001US-272751P
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                                                                                                                                                                                                                                                Fritz LC, Burrows FJ;
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Matches 416; Conserv
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                                                    WO200269900-A2.
                  Homo sapiens.
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301 FEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
                                                                       LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQHQHLLQKHLLSACFRNE 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Deltan isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopolesis, muscle wasting (e:g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAX5593-64), polynucleotides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell regulatory protein; p63; huTAp63 beta; TAp63 beta; human;
                                                                                                        cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cell regulatory protein p63, isoform huTAp63 beta.
                                                                                                                                                                                                                 421 LVEPRRETPKQSDVFFRHSKPP 442
                                                                                                                                                                                                                                                              : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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97US-0062076.
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15-OCT-1997;
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Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient \cdot
        WPI; 2000-628399/60.
N-PSDB; AAC66033.
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                                                                           1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                     SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP
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                                                                                                                                                                                                                                                                         Gaps
identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.
                                                             16;
                                             Length 516;
                                                             Indels
                                             91.7%; Score 2185; DB 20; 94.1%; Pred. No. 5.1e-189; ive 3; Mismatches 7;
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99US-0466396.
99US-0476496.
2000US-0480884.
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Matches 416; Conservative
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17-DEC-1999;
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10-JAN-2000;
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                                                               comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient er tracted with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
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                                             This invention describes a novel isolated polypeptide (I) which
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                                                                                                                                                                                                                                                                                                                                                                 Length 516;
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Pred. No. 5.1e-189;
3; Mismatches 7;
Disclosure; Page 255-256; 261pp; English
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94.1%;
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1 MSQSTQTNEFLSPEVFQHIW......PRQSDVFFRHSKPPNRSVYP 448
GenCore version 5.1.6
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	-643	909-	-643	-542	909-	-643	-542	909-	-643	-542	-09-606-421B	-09-277-196-19	-09-643-597-343	-542	-09-606-421B-3	-09-643-597-34	-09-277-196-2	-542	909-	-643	-542	909-	-643	-480	-542	909-
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28 1297.5 54.4 420 4 US-09-27 30 1297.5 54.4 635 4 US-09-08 30 1 722.5 30.3 393 1 US-08-99 31 722.5 30.3 393 1 US-08-99 32 722.5 30.3 393 1 US-08-99 33 722.5 30.3 393 1 US-08-08 34 722.5 30.3 393 1 US-08-09 35 717.5 30.3 393 1 US-08-09 36 717.5 30.1 393 1 US-08-39 41 717.5 30.1 393 1 US-08-39 42 717.5 30.1 393 1 US-08-39 44 717.5 30.1 393 1 US-08-39 44 717.5 30.1 393 1 US-08-39 44 717.5 30.1 393 1 US-08-39 45 717.5 30.1 393 1 US-08-39 46 717.5 30.1 393 1 US-08-39 47 717.5 30.1 393 1 US-08-39 48 717.5 30.1 393 1 US-08-39 49 717.5 30.1 393 1 US-08-39 48 717.5 30.1 393 1 US-08-39 49 717.5 30.1 393 1 US-08-39 48 717.5 30.1 393 1 US-08-39 49 717.5 30.1 393 1 US-08-39 41 717.5 30.1 393 1 US-08-39 42 717.5 30.1 393 1 US-08-39 43 717.5 30.1 393 1 US-08-39 44 717.5 30.1 393 1 US-08-39 45 717.5 30.1 393 1 US-08-39 46 717.5 30.1 393 1 US-08-39 47 717.5 30.1 393 1 US-08-39 48 717.5 30.1 393 1 US-08-39 49 PELICANT: Wang, Tongtong APPLICANT: Bangur, Chaitanya S. APPLICANT: Honderson, Nancy APPLICANT: Honderson, Nancy APPLICANT: Honderson, Nancy APPLICANT: Honderson, Nancy UNRBER US-09-643. CUNRENT FILING DATE: 2000-08-12 NUMBER OF END NOS: 369 2007WAREN FILING DATE: 2000-08-12 UNGRANISM: Homo sapiens 10-643-597-340 2004 1	Sequence 20, Appl Sequence 3, Appli Sequence 27, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 26, Appli Sequence 26, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 7, Appli	R THE THERAPY	4; Length 448; 18; 0; Indels 0; Gaps 0; VDEPSEDGATNKIEISMDCIRMO 60
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Fanger, Gary R.
Li, Samuel X.
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Best Local Similarity 100.
Matches 448; Conservative
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                                                                                                  GENERAL INFORMATION:
                                                             US-09-606-421B-340
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US-09-643-597-344
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 100.0%; Score 2383; DB 4; Best Local Similarity 100.0%; Pred. No. 3.6e-218; Matches 448; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                APPLICANT: Fan, Ligun
APPLICANT: Fan, Ligun
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CATTLE OF INVENTION: AND DIAGNOSIS OF LUNG CURRENT FILLING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastseQ for Windows Version 3.0
LENGTH: 448
TYPE: PRT
                                                                                                                                    LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
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                                                                                                                                                 Sequence 340, Application US/09542615A Patent No. 6518256 GENERAL INFORMATION:
                                                                                                                                                                                                                                                          APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-542-615A-340
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US-09-542-615A-340
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61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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                                                                                                                                                                                                                                                                                                                  APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 3.6e-218;
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LVEPRRETPKQSDVFFRHSKPPNRSVYP
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Patent No. 6426072
GENERAL INFORMATION:
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya
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9 9 240 240 300 300 360

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us-09-538-106-15.rai

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61 DSDLSDPWWPQYTNLGLLNSWDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455c9
CURRENT APPLICATION NUMBER: US/09/606,421B
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                           Score 2185; DB 4;
Pred. No. 3.1e-199;
3; Mismatches 7;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C8
                             CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SSCTWARE: FastSEQ for Windows Version 3.0
ERQ ID NO 344
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Best Local Similarity 94.1%;
Matches 416; Conservative
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Bangur, Chaltanya
Hosken, Nancy
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael I
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.
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                                                                                                                                                      ) ORGANISM: Homo sapiens
US-09-542-615A-344
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                      APPLICANT: Raids, Michael D.
APPLICANT: Raids, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Amuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aljun
APPLICANT: McHaerson, Robert A.
APPLICANT: McHaerson, Robert A.
APPLICANT: Howelll, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: LENTH: 516
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Pred. No. 3.1e-199;
3; Mismatches 7;
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APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS A
            Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Wancy
Fanger, Gary R.
Li, Samuel X.
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94.18;
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Matches 416; Conservative
Wang, Tongtong
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                       1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
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Pred. No. 4.3e-199;
3; Mismatches 7;
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Banger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOF
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: 2000-04-14
NUMBER OF SEQ ID NOS: 350
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Local Similarity 94.1%;
les 416; Conservative
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US-09-542-615A-339
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APPLICANT: Wang, To
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Rang, Wichael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Cary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aljun
APPLICANT: Menderson, Robert A.
APPLICANT: Moreill, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND INGENERIC S.
TITLE OF INVENTION: COMPOSITIONS AND INGENERIC S.
TITLE OF SEQ ID NOS: 2000-08-21
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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                                                     Length 516;
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                                               Score 2185; DB 4;
Pred. No. 3.1e-199;
3; Mismatches 7;
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                                                   91.7%;
94.1%;
                                                 Query Match
Best Local Similarity 94.1
Matches 416; Conservative
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; ORGANISM: Homo sapiens
US-09-606-421B-344
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US-09-643-597-339
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Matches 416; Conserv
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aljun
APPLICANT: Henderson, Robert A.
APPLICANT: Moneill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FLIE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
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FastSEQ for Windows Version 3.0
                                                                                                LVEPRRETPKQSDVFFRHSKPP 442
                                                                                                                Sequence 342, Application US/09643597
Patent No. 6426072
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Fan, Ligun
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SOFTWARE: FASTSEQ for
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APPLICANT:
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Lidgun
APPLICANT: Fan, Lidgun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Seken, Nancy
APPLICANT: Wang, Aljun
APPLICANT: Wasir A.
FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/66,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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94.1%; Pred. No. 4.3e-199;
iive 3; Mismatches 7;
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Matches 416; Conservative
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; ORGANISM: Homo sapiens
US-09-606-421B-339
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US-09-606-421B-339
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APPLICANT: Ralos, Michael D.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILLING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
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Pred. No. 4.7e-199;
3; Mismatches 7;
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                                                                                                  Sequence 342, Application US/09542615A Patent No. 6518256 GENERAL INFORMATION:
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APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun
                  421 LVEPRRETPKQSDVFFRHSKPP 442
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Best Local Similarity 94.1%;
Matches 416; Conservative
                                                                                                                                             APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
APPLICANT: Kalos, Michael
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US-09-542-615A-342
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LENGTH: 680
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                                                                                                       APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIGGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEC ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6476206
GENERAL INFORMATION:
APPLICANT: Trink, Barry
APPLICANT: Trink, Barry
APPLICANT: Saforniski, Edward
APPLICANT: Ratovitski, Edward
APPLICANT: Ratovitski, David
TITLE OF INVENTION: p40 Protein Acts as an Oncogene
FILE REFERENCE: 01107.79765
                                                                                                                                                                                                                                                                                                                                                                                                                Score 2185; DB 4;
Pred. No. 4.7e-199;
3; Mismatches 7;
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CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/079736
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 20
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94.18;
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Best Local Similarity 94.19
Matches 416; Conservative
                                         Fanger, Gary R.
Li, Samuel X.
                      Hosken, Nancy
                                                                                       Wang, Aijun
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Query Match
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                 Best Local
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                                                                                                                          Gaps
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APPLICANT: Wang, Trongtong
APPLICANT: Fan, Liqun
APPLICANT: Raios, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Losamell X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mendelson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Honderson, Robert A.
APPLICANT: Honderson, Robert A.
APPLICANT: McNeill, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.121.455cll
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ IO NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 426;
                                                                                                  le-194;
                                                                                            89.6%; Score 2136; D. Larity 93.1%; Pred. No. 1e-1
Conservative 5; Mismatches
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 19 LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 343, Application US/09643597 Patent No. 6426072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPKQSDVFFRHSKPP 442
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                                      TYPE: PRT
CORGANISM: Homo sapiens
US-09-277-196-19
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                                                                                                         Best Local Similarity
Matches 405; Conserv
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                                                            70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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                                                                                                                                                                                PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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                                 Gaps
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                                 16;
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 Length 461;
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                               Indels
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Pred. No. 6.2e-164;
3; Mismatches 7;
   ; DB 4;
6.2e-164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fan, Liquin APPLICANT: Ralos, Michael D. APPLICANT: Bangur, Chaitanya S. APPLICANT: Hosken, Nancy A. APPLICANT: Fanger, Gary R. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THI FILE REFERENCE: 210121.455C8
Score 1813; DE
Pred. No. 6.2e-
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 343, Application US/09542615A Patent No. 6518256
                              3;
76.1%;
93.0%;
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Best Local Similarity 93.0%;
Matches 347; Conservative
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                              Matches 347; Conservative
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Fan, Liqun
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              Similarity
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APPLICANT: Wang, To
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US-09-542-615A-343
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QY	250 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP 309
qa	195 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP 254
Qy	310 GRDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIOMTSIKKRRSPDDELLYLPVRGR.369
qa	255 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 314
δλ	370 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSACFRNELVEPRRETP 429
අු	315 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQHLLQKQTS 358
Qy	430 KOSDVEFRHSKPP 442
qa	359 IQSPSSYGNSSPP 371
Search Job tim	Search completed: August 7, 2003, 09:54:52 Job time : 13.3586 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:
August 7, 2003, 09:46:34; Search time 19.1264 Seconds

(without alignments)
2781.719 Million cell updates/sec
Title:
US-09-538-106-15
Sequence:
1 MSOSTQTNEFLSPEVFQHIW......PKQSDVFFRHSKPPNRSVYP 448
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
451899 seqs, 118759770 residues
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description

No. Score Match Length DB ID Description

2 2383 100.0 448 10 US-09-850-716A-340 Sequence 340, App 2 2383 100.0 448 10 US-09-850-716A-340 Sequence 340, App 4 2185 91.7 516 10 US-09-850-716A-340 Sequence 344, App 5 2185 91.7 516 10 US-09-850-716A-344 Sequence 344, App 6 2185 91.7 516 10 US-09-850-716A-344 Sequence 344, App 7 516 10 US-09-850-716A-349 Sequence 344, App 8 2185 91.7 641 10 US-09-850-716A-339 Sequence 339, App 1 2185 91.7 641 10 US-09-850-716A-339 Sequence 339, App 1 2185 91.7 680 10 US-09-850-716A-339 Sequence 342, App 1 2185 91.7 680 10 US-09-850-716A-342 Sequence 342, App 1 2185 91.7 680 10 US-09-850-716A-342 Sequence 342, App 1 2185 91.7 680 10 US-09-850-716A-342 Sequence 342, App 1 2185 91.7 680 10 US-09-850-716A-342 Sequence 342, App 1 2185 91.7 680 10 US-09-850-716A-342 Sequence 342, App 1 2185 91.7 680 10 US-09-850-716A-342 Sequence 342, App 1 2185 91.7 680 10 US-09-850-716A-342 Sequence 343, App 1 2181 76.1 461 10 US-09-850-716A-343 Sequence 343, App 1 2181 76.1 461 10 US-09-850-716A-343 Sequence 343, App 1 2181 76.1 461 10 US-09-850-716A-343 Sequence 343, App 1 2181 76.1 461 10 US-09-850-716A-343 Sequence 343, App 1 2 2185 91.7 680 10 US-09-850-716A-343 Sequence 343, App 1 2 2185 91.7 680 10 US-09-850-716A-342 Sequence 343, App 1 2 2185 91.7 680 10 US-09-850-716A-343 Sequence 343, App 1 2 2185 91.7 680 10 US-09-850-716A-343 Sequence 343, App 1 2 2185 91.7 680 10 US-09-850-716A-343 Sequence 343, App 1 2 2185 91.7 680 10 US-09-850-716A-343 Sequence 343, App 1 2 2185 91.7 680 91.7 68

Sequence 343, App	141, 1	Sequence 341, App	3,4	Sequence 2, Appli	Sequence 338, App	Sequence 338, App	33	М,	Sequence 152, App	Sequence 152, App	Sequence 152, App	-	Sequence 3, Appli	Sequence 10, Appl	Sequence 32, Appl		6	4	Sequence 9, Appli	Sequence 4, Appli	'n	Sequence 2, Appli	78,	Sequence 6, Appli	34,	'n	4		Sequence 28, Appl
0 US-09-897-778-343	US-09-735-705-341	0 US-09-850-716A-341	0 US-09-897-778-341	5 US-10-274-874-2	US-09-735-705-338		0 US-09-897-778-338	US-09-735-705-152	0 US-09-850-716A-152	0 US-09-897-778-152	1 US-09-466-396A-152	5 US-10-274-874-20	4 US-10-155-059-3	0 US-09-732-384-10	US-09-776-695-32	0 US-09-732-384-3	0 US-09-860-211-9	1 US-09-029-327-4	1 US-09-860-286-9	5 US-10-274-874-4	5 US-10-160-290-2	5 US-10-076-691-2	5 US-10-146-473-78	5 US-10-038-010-6	0 US-09-968-851-34	5 US-10-160-290-3		0 US-09-968-851-36	0 US-09-968-851-28
61 10	156 9	156 10	156 10	156 15	6 989	86 10		86 9	386 10	386 10	86 11	120 15	35 14	36 10	193 9	103 10	193 10	13 11	393 11	193 15	193 15	128 15	153 15	390 15	-	П	П	181 10	374 10
	75.4		75.4	75.4	75.4	75.4	75.4	75.1	75.1		75.1	54.4	54.4	54.4	30.1	30.1	30.1	30.1	717.5 30.1	30.1	30.1	30.1	30.1		30.0	29.8	29.6	29.5	
16	17	18	19	70	21	22	73												35 7.										45 6

ALIGNMENTS

US-09-735-705-340

| Sequence 340, Application US/09735705 |
| Sequence 340, Application US/09735705 |
| Sequence 340, Application US/09735705 |
| Setent No. US2002005232941 |
| GENERAL INFORMATION: |
| APPLICANT: Wang, Tongtong |
| APPLICANT: Ean, Lidual D. |
| APPLICANT: Bangur, Chaitanya S. |
| APPLICANT: Honger, Cary R. |
| APPLICANT: Honger, Cary R. |
| APPLICANT: Wang, Aijun |
| APPLICANT: Mang, Aijun |
| APPLICANT: Mang, Aijun |
| APPLICANT: Momell, Particia D. |
| APPLICANT: Momble No. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
| FILE REFERENCE: 210121.455614 |
| CURRENT APPLICATION NUMBER: US/09/735,705 |
| CURRENT FILING DATE: 2000-12-12 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 340 |
| TYPE: PRT |
| TYPE: PRT |
| OKGANISM: Homo sapiens |

Query Match 100.0%; Score 2383; DB 9; Length 448; Best Local Similarity 100.0%; Pred. No. 1e-208; Matches 448; Conservative 0; Mismatches 0; Indels 0

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Qy 301 FEARICACPGRDRKADEDSIRKQOVSDSTRNGDGTKRPFRONTHGIQMTSIKKRRSPDDE 360		DESTRUCTION 1 MSG01QINEFLSPEVEQHIMMOFLEQPICSVQFILLENFVDEPERGAINNIELSMUCIRMQ	Db 121 SPSPAIPSNTDYPGPHSEDVSFQGSTAKSATWIYSTELKKLYCQIAKTCPIGITITITITITITITITITITITITITITITITITITI	241 ITGROSVLVPYEPPQVGTEFTTVLYNEWNOOVGGRANRRPILLIYTLETROGYLGRRC 301 FEARICACPGRDEKADEDSIRKQOVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 11111111111111111111111111111111111
0.00 0.00	6A-340 40, App 40, App 0S2002	VS-09-800-716A-340 US-09-800-716A-340 Query Match Best Local Similarity 100.0%; Pred. No. 1e-208; Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OV 1 MSOSTOTNEFLSPEVFOHTWDFLEOPTICSVOPTDI.MFVDEPSERGATNKTETSMR-01800.	INCOMES AND ADDITIONAL TO A STANDARD AND ADDITIONAL THROUGH AND AD	QY 121 SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPP 180

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US-09-850-716A-344
                                                                                                                                                                            SEQ ID NO 344
LENGIH: 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRC 300
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larity 94.1%; Pred. No. 1.4e-190;
Conservative 3; Mismatches 7; Indels 1
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                                                                                                                                 APPLICANT: Rauls, Augus APPLICANT: Ralos, Michael D. APPLICANT: Ralos, Michael D. APPLICANT: Bangur, Chaltanya S. APPLICANT: Bangur, Chaltanya S. APPLICANT: Bosken, Nancy APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Wang, Aijun APPLICANT: Weng, Aijun APPLICANT: Henderson, Robert A. APPLICANT: Moneill, Particia D. APPLICANT: Moneill, Particia D. APPLICANT: Panger, Neil TILLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: EastSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
                         448
              LVEPRRETPKQSDVFFRHSKPPNRSVYP
LVEPRRETPKQSDVFFRHSKPPNRSVYP
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Patent No. US20020052329A1
GENERAL INFORMATION:
                                                                                                                        Wang, Tongtong
Fan, Liqun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo saplens
US-09-735-705-344
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Matches 416; Conserv
                                                             RESULT 4
US-09-735-705-344
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                                      GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Macuel D.
APPLICANT: Retuer, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: CAND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455215
CURRENT PILLING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Peckham, David W.
APPLICANT: Fanger, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 1.4e-190;
3; Mismatches 7;
Sequence 344, Application US/09850716A Patent No. US20020115139A1
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APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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94.18;
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Best Local Similarity 94.1;
Matches 416; Conservative
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us-09-538-106-15.rapb

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Sequence 339, Application US/09850716A Patent No. US20020115139A1 GENERAL INFORMATION:
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94.18;
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Best Local Similarity 94.1
Matches 416; Conservative
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Matches 416; Conservative
                                   sapiens
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                 TYPE: PRT
ORGANISM: HOMO
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APPLICANT: Fail, Light
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45514
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                         16;
                                                                                                                                                              Length 516;
                                                                                                                                                                                         Indels
                                                                                                                                                          Score 2185; DB 10;
Pred. No. 1.4e-190;
3; Mismatches 7;
FILE REFERENCE: 210121.455C16
CURRENT PPLICATION NUMBER: U5/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTHARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 344
LENGTH: 516
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Patent No. US20020052329A1
GENERAL INFORMATION:
                                                                                                                                                           Query Match 91.7%;
Best Local Similarity 94.1%;
Matches 416; Conservative
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Fan, Ligun
                                                                                                                ; ORGANISM: Homo sapiens
US-09-897-778-344
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APPLICANT:
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                                                                            DSDLSDPMWPQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
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    Length 641;
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                                         Indels
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APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455615
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT APPLICATION NUMBER: 2001.05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
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94.1%; Pred. No. 2e-190;
ive 3; Mismatches 7;
Score 2185; DB 9;
Pred. No. 2e-190;
3; Mismatches 7;
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ATWTYSTELKKLYCQIAKTCPIQIKVWTPP 180
           SSCVGGMNRRPILIIVTLETRDGQVLGRRC 300
                                      NGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360
                                                                                SREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
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SSCVGGMNRRPILIIVTLETRDGQVLGRRC 300
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2.1e-190;
hes 7; Indels 16; Gaps
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G CANCER
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US20020147143A1
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                                                                                                                                                                                                 Sequence 342, Application US/09850716A
Fatent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: RAIOS, Michael D.
APPLICANT: Mchael D.
APPLICANT: Mchael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 680;
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                                                                                                                    421 LVEPRRETPKQSDVFFRHSKPP 442
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US-09-850-716A-342
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US-09-897-778-342
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                                                                      APPLICANT: Faulyer, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Wederson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Nell
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: 2010.10.5/09/897,778
CURRENT FILLING DATE: 2001-06-28
CURRENT FILLING DATE: 2001-06-28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
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Pred. No. 2.1e-190;
3; Mismatches 7;
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Publication No. US20030113774A1

GENERAL INFORMATION:
APPLICANT: Trink, Barry
APPLICANT: Jen, Jin
APPLICANT: Satovitski, Edward
APPLICANT: Sidransky, David
TITLE OF INVENTION: P40 Protein Acts as an Onc
FILE REPERENCE: 01107.79965
CURRENT APPLICATION NUMBER: US/10/274,874
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APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
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Best Local Similarity 94.1%;
Matches 416; Conservative 3
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FastSEQ for Windows Version 3.0
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US-09-850-716A-343
; Sequence 343, Application US/09850716A
; Patent No. US20020115139A1
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Best Local Similarity 93.0%;
Matches 347; Conservative
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359 IQSPSSYGNSSPP 371
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Matches 347; Conservative
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US-09-850-716A-343
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LENGTH: 461
SOFTWARE: F
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APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Honsen, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aljun
APPLICANT: Panger, Nebert A.
APPLICANT: Panger, Nell
APPLICANT: APPLICANT: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFRENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                           Length 426
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                         Score 2136; DB 15;
Pred. No. 3.1e-186;
5; Mismatches 9;
          PRIOR APPLICATION NUMBER: US/09/277,196
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079736
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 3.0
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 2002-10-22
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Best Local Similarity 93.1%;
Matches 405; Conservative
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Fan, Liqun
                                                                                                                                                        ORGANISM: Homo sapiens
CURRENT FILING DATE:
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US-09-735-705-343
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                                                                                                                            LENGTH: 426
TYPE: PRT
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                                                                                70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                195 PYEPPQVGTEFTTVLYNFWCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                            PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                             250 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 461;
Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE ERFERENCE: 210121.455015
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FESTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1813; DB 10;
Pred. No. 9.8e-157;
3; Mismatches 7;
76.1%; Score 1813; DB 9;
93.0%; Pred. No. 9.8e-157;
tive 3; Mismatches 7;
```

Qy	190	190 PVYKKAEHVTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
qq	135	PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV. 194
δy	250	250 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACP 309
qo	195	PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP 254
Οy	310	310 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 369
qq	255	255 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 314
οy	370	370 ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQHQHLLQKHLLSACFRNELVEPRRETP 429
QQ	315	- H
. VO	430	430 KOSDVFFRHSKPP 442
Db	359	359 IQSPSSYGNSSPP 371
Search	complet	Search completed: August 7, 2003, 09:57:08

Search completed: August 7, 2003, 09:57:08 Job time: 20.1264 secs

```
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
```

OM protein - protein search, using sw model

August 7, 2003, 09:42:03; Search time 14.1241 Seconds (without alignments) 3050.350 Million cell updates/sec Run on:

US-09-538-106-15

2383 1 MSQSTQTNEFLSPEVFQHIW......PKQSDVFFRHSKPPNRSVYP 448 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cellular tumor ant	tumor suppressor p	cellular tumor ant	tumor suppressor p	cellular tumor ant	Bassoon protein -	hypothetical prote	transcription fact	proline-rich pepti	polyketide synthas	DHR39-short protei	nuclear steroid/th	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	hypothetical prote	⊂	syndecan precursor	hypothetical prote	flocculation suppr	hypothetical prote								
ID.	JH0631	A29376	S02193	S51648	S02192	JH0633	DNHU53	DNMS53	S06594	JC6176	S38824	JC6193	146226	T42730	T32008	A56923	A41819	C69679	S33709	S33708	D54689	C54689	A56178	T31782	A56922	A54949	I49528	S61694	T06635
DB	Н	Н	Н	Н	Н	Н	Н	-	-	7	7	~	7	7	~	7	N	~	Н	-	Н	7	~	7	7	7	~	Н	7
Length	368	363	367	386	391	386	393	390	393	393	381	391	77	3942	1819	2529	5762	4273	701	808	1691	1894	1912	631	2578	395	384	166	606
% Query Match	9.6	9.	7.	-:	7.0			0.0	0.0	5.5	5.		6.0	8.	1.7	9.	9.	9.	9.	9.	5.5	4.5	4.5	4.5	5.5	4.	4.4	7.	4.
Ma Ka	ě	'n	m	'n	ĕ	30	ĕ	ř	ñ	Ñ	Ñ	čί	Ä	•	•	•	•	•	•	•	•	•	•	•			•	•	•
Score	847.5	777.5	764.5	741.5	732	719.5	717.5	715	714.5	704	702	699.5	259.5	114.5	111.5	110.5	110	109	108.5	108.5	107	107	107	106.5	106.5	105.5	105	105	105
Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

PGRDRKADEDSIRKQQ----VSDSTKNGDGTKRPFRQ-NTHGIQMTSIKKRRS----PDDE 360

309

qq δy g ò qq

SNF2 protein - yea LTR gag/pol polypr	protein C43E11.3 { hypothetical prote	HF-1 regulatory el mycelial surface a	hypothetical prote hypoxia-inducible	hypothetical prote hypothetical prote	GTPase-activating A-kinase anchor pr	Bassoon protein : hypoxia-inducible	hypothetical prote zinc finger protei
S15047 T01397	B87754 T00344	A48143 T17415	S19150 JC4851	T24447 T51372	S27809 T03094	T42761 JC7619	T15264 T14273
0.0	00	77	~ ~	77	0 0	~ ~	77
1703 1456	1590	780	628 1505	600 526	1165	3938	1621
4. 4	4 4.	4.4	4.4 6.2	4 4	4 4 2 2	4.4	4.4
104.5	104	102.5	102 100.5	100 99.5	99.5	99.5	666
30	335	34 35	36	38 30 8	40 41	4 4 2 8 3	44

ALIGNMENTS

RESULT 1

	JH0631	
	cellular tumor antigen p53 - rainbow trout	ut
	C;Species: Oncorhynchus mykiss (rainbow trout) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	trout) 0-Sep-1999 #text_change 10-Sep-1999
	C; Accession: JH0631	
	R; de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T	, A.; Baney, C.; May, P.; Soussi, T.
_	Gene 112, 241-245, 1992	
	A)TILLE: Kainbow Troug bys: CDNA cioning and blochemical characterization	and blochemical characterization.
	A; Reference number: JH0631; MOID: 9ZZIU006; FMID: 133936Z	0; PMID:133930Z
	A; Molecule type: mRNA	
	A; Residues: 1-396 <def></def>	
	A; Cross-references: GB:M/0145; NID:g213828; PIDN:AAA49605.1; PID:g213829	28; PIDN:AAA49605.1; PID:9213829
	C.Comment: This protein is the product of a	f a timor suppressor depends whose inactiv
	C;Superfamily: cellular tumor antiqen p53	3
	C; Keywords: apoptosis; cell division control	trol; DNA binding; homotetramer; nucleus; pho
	F;164,167,227,231/Binding site: zinc (Cys, E F;395/Binding site: phosphoryl-RNA (Ser) (co	F;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
	Query Match 35.6%; Score 847.5; DB 1;	847.5; DB 1; Length 396;
•	Best Local Similarity 45.4%; Pred. No. 7.5e-58; Matches 181; Conservative 61; Mismatches 102;	
	QY 11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDE	11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70
	Db 12 LSQESFEDLW	12 LSQESFEDLWSWV 39
	QY 71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHA	QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS 128
	DD 40 GYDNFWEFDPS	
	QY 129 NTDYPGPHSFDVSFQQSSTAKSATWTYSTE	YSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA 188
	Db 88 TSDYPGALGFQLRFLQSSTAKSVTCTYSPD	88 TSDYPGALGFQLRFLQSSTAKSVTCTYSPDLNKLFCQLAKTCPVQIVVDHPPPPGAVVRA 147
	Qy 189 MPVYKKAEHVTEVVKRCPNHELSREFNEGQ	MPVYKKAEHVTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAOYVEDPITGROSVL 248
	Db 148 LAIYKKLSDVADVVRRCPHHQSTSENNEGP	
	QY 249 VPYEPPQVGTEFTTULYNFMCNSSCVGGMN	VPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICAC 308
	Db 207 VPYEPPQVGSECTIVLYNFMCNSSCMGGMN	207 VPYEPPQVGSECTTVLYNFMCNSSCMGGMNRRPILTITTETQEGQLLGRRSFEVRVCAC 266

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Cypecies: Gallus gallus (chicken)
Cypecies: Gallus gallus (chicken)
Cypecies: Gallus gallus (chicken)
Cypecies: 302193
Cypecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
Cyccession: 302193
Cycussi, T.; Beque, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A.71tile: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A.74tile: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A.74cession: 302193
A.74cession: 302193
A.76cession: 502193
A.76cession: 502193
A.76cession: 502193
A.76cession: 502193
A.76cession: 502193
Cycoperfamily: cellular tumor antigen p53
Cycoperfamily: cellular tumor antigen p53
Cycoperfamily: cellular tumor antigen p53
Cycoperfamily: cellular tumor control; DNA binding; homotetramer; nucleus; pho Cycoperfamily: 228/Bahnding site: 21nc (Cys, His, Cys, Cys) #status predicted
F:366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyaccesion: S51648
Rybequiedt, F.; Willems, L.; Burny, A.; Kettmann, R.
submitted to the EMBL Data Library, September 1994
A; Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and it A; Reference number: S51648
A; Reference number: S51648
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-386 < DEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
C; Superfamily: cellular tumor antigen p53
C; Superfamily: cellular tumor antigen p53
C; Reywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote F; 168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) *status predicted F; 385/Binding site: phosphoryl-RNA (Ser) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LEPTEVFWDLWSMLPY---SMQQL------PLPEDHSNWQELS----PLEPSDPPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LSP-EVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.1%; Score 764.5; DB 1; Best Local Similarity 44.6%; Pred. No. 1.8e-51; Matches 169; Conservative 50; Mismatches 105;
                                        N; Alternate names: nuclear oncoprotein p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRETYEMLLKIKESLELMQ 386
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GRRRYEMLKEINEALQLAE 335
cellular tumor antigen p53 - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellular tumor antigen p53 - bovine
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                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein A;Reference number: A29376; MUID:88143684; PMID:2830576
A;Accession: A29376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph
F;150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; PID:g64962
R;Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A;Title: Overaxpression of Wild-type p53 interferes with normal development in Xenopus A;Reference number: 151639; MUID:94134403; PMID:8302570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 DALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                 cellular tumor antigen p53 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Decies: Xenopus laevis (African clawed frog)
C;Accesion: A29376; S61531; S72313; I51639
C;Accession: A29576; S61531; C.C.; Mechall, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQSTQTNEFLSPEVFQHIWDFLEQPI----CSVQPIDLNFVDEPSEDGATNKIEISMDCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-293,295-363 <HOE>
A;Cross-réferences: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
A;Cross-réferences: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSETGMDPPLSQETFEDLWSLLPDPLQTVTCRLDNLS-EFPDYP-----LAADMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
A;Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.6%; Score 777.5; DB 1; Length 3 Best Local Similarity 42.5%; Pred. No. 1.7e-52; Matches 171; Conservative 55; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|: | ::|| |||: |: :|| | : || : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S72313
A; Accession: S72313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-363 <SOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S61531
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Length 386;

DB 1;

Score 741.5;

31.1%;

Query Match

RESULT S02193

	4 .	
11 LSFEVEQHIMDELEQPICSVQPIDENFVDEPSEDGATNKIEISMDCIRMQDSDLSDPWWP 70	QY 61 DSDLSDPWMPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL	SVTAPSPYAQPSSTEDAL 120 : : APAPVAPASATPWPL 91
71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA 125 	QY 121 SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVWTPP	COIAKTCPIQIKVMTPP 180 : : : : : COLAKTCPVQLWVTSTP 149
126IPSNTDYPGPHSFDVSFQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ 182 :	QY 181 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGG-IAPPSHLIRVEGNSHAQYVED	SHLIRVEGNSHAQYVED 239
OY 183 GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGGIAPPSHLIRVEGNSHAQYVEDPIT 242 :	QY 240 PIJGRQSVLVPXEPPQVGTEFTYLXNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRR	JIIVTLETRDGQVLGRR 299 : :
243 GRQSVLVPYEDPQVGTEFTTVLXNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE 302 	QY 300 CFEARICACPGRDKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-D	HGIQMTSIKKRSP-D 358
303 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL 361 1 1 1 1 1 1 1 1 1	Qy 359 DELLYLPVRGRETYEMLLKIKESLEL 384 	
362 LYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQH-QHLLQKHLLS-ACFRN 419 		
420 ELVEPRRETP 429 :: : 376 PMLKREGP 383	cellular tumor antigen p53 - golden hamster N;Alternate names: tumor-suppressor protein p53 C;Species: Mesocricetus auratus (golden hamster) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change	change 10-Sep-1999
SO2192 cellular tumor antigen p53 - rat N:Alternate names: gene p53 protein; nuclear oncoprotein p53 C:Species: Rattus norvegicus (Norway rat) C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	R;Legros, Y.; McIntyre, P.; Soussi, T. Gene 112, 247-250, 1992 A;Title: The CDNA cloning and immunological characterization of hamster A; Reference number: J40633; MUID:92210007; PMID:1555773 A;Accession: J40633 A;Molecule type: mRNA A;Residues: 1-396 <-1287 A;Residues: 1-396 <-1287 A;Coss.references: GR:M75144: NID:0191414: PIDN:AAA37085.1: PID:019141	ion of hamster p53. 1: prD:g191415
R;Soussi, T.; de Fromentel, C.C.; Breugnot, C.; May, E. Nucleic Acids Res. 16, 11384, 1988 A;Title: Nucleotide sequence of a CDNA encoding the rat p53 nuclear oncoprotein. A;Reference number: S02192; MUID:89083585; PMID:3060862 A;Accession: S02192; MUID:89083585; PMID:3060862 A;Molecule type: mRNA A;Residues: 1*391 <sou></sou>	A; Experimental Source: Kidney, Strain MPI C; Genetics: A; Genetics: C; Superfamily: cellular tumor antigen p53 C; Superfamily: cellular tumor antigen p53 C; Superfamily: apoptosis; cell division control; DNA binding; homotetramer; nucleus; F: 179, 182, 241, 245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F; 395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted	homotetramer; nucleus; pho #status predicted
NOSS-TENERGES: EMBL:X13/1058; NID:GD6828; PIDN:CAA31457.1; PID:G56829 ulla, J.E.; Schneider, R.P. leic Acids Res. 21, 713-717, 1993 Lite: Structure of the rat p53 tumor suppressor gene. eference number: 841149; MITD: 93187268; DMTD: 8441680	Query Match 30.2%; Score 719.5; DB 1; Ler Best Local Similarity 38.1%; Pred. NO. 6e-48; . Matches 162; Conservative 67; Mismatches 145; Inc	Length 396; Indels 51; Gaps 8;
ccession: S41149 tatus: preliminary; nucleic acid sequence not shown; translation not shown leading type: DNA 75-301 / WILLS pesidings: 1-173 'W' 175-301 / WILLS	QY 11 LSPEVFQHIMDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPP	4DCIRMQDSDLSDPMWP 70 : : LPSSDSIEELFL 46
ross references: EMBL:L07909 Ote: the nucleotide sequence was submitted to the EMBL Data Library, December 1992 enetics: 25/2: 32/3: 123/3: 128/1: 259/2: 305/1: 329/3: 365/7	QY 71 QYTNLGLLNSMDQOLQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSSPAIPSNT D 1	SSTFDALSPSPAIPSNT 130
uperfamily: cellular tumor antigen p53 uperfamily: cellular tumor antigen p53 ewords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosph 74,177,236,240/Binding site: zinc (cys, His, Cys, Fatatus predicted 90/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted	QY 131 DYPGPHSEDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAMP	KKVMTPPPQGAVIRAMP 190
Query Match 30.7%; Score 732; DB 1; Length 391; Best Local Similarity 42.0%; Pred. No. 6.38-49; Matches 162; Conservative 64; Mismatches 116; Indels 44; Gaps 11; 2 SQSTQTNEF-LSPEVFQHIWDFLEQPICSYQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60	QY 191 VYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGROSVLVP 115 111111111111111111111111111111111	AQYVEDPITGROSVLVP 250 : :: : \text{REYLDDKQTFRHSVVVP 222} \text{SVIGRECFEARICACPG 310} :

```
A; Residues: 1-71,'P', 73-272,'H',274-393 < HAR>
A; Residues: 1-71,'P', 73-272,'H',274-393 < HAR>
A; Cross-references: GB: K03199; NID: 0489478; PIDN: AAA59989.1; PID: 9189479
A; Experimental source: clone pR4-2, cell line A431
B; Harris, N.; Brill. E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V. Mol. Cell. Biol. 6, 4650-4656, 1986
A; Title: Molecular basis for heterogeneity of the human p53 protein.
A; Reference number: A93086; MUID: 87089826; PMID: 3025664
A; Accession: A25397
A; Molecule type: mRNA
A; Residues: 178, T', 80-393 < HARI>
A; Residues: 178, T', 80-393 < HARI>
A; Residues: 178, T', 20-393 < HARI>
A; Residues: BMBL: M14694; NID: 9339813; PIDN: AAA61211.1; PID: 9339814
A; Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: 138083
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-189, 'LESILSEWKEICVWSIWMTETLFDIVWWCPMSRLRLALT','VPPSTTTCVTVPAWAA'
A;Cross-references: EMBL;X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A;Note: deletion of a C nucleotide causes a frameshift at position 566
A;Accession: 138083
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A;Status: translated from GB/EMBL/DDBJ
A;Reledues: 1-247,'Q',249-393 <F06>
A;Residues: 1-247,'Q',249-393 <F06>
A;Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443
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A;Residues: 1-71,'P',73-237,'Y',239-393 <F07>
A;Cross-references: EMBL:X60016; NID:9506444; PIDN:CAA42631.1; PID:9506445
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A; Residues: 1-192, 'R', 194-393 <F02>
A; Cross-references: EMBL:X60011; NID:9506434; PIDN:CAA42626.1; PID:9506435
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A;Molecule type: mRNA
A;Residues: 1-455,'T',247-393 <F04>
A;Cross-references: EMBL:X60013; NID:9506438; PIDN:CAA42628.1;
A;Accession: I38086
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-393 <F03>
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A; Molecule type: mRNA
A; Residues: 1-236,'I',238-393 <F05>
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A;Status: translated from GB/EMBL/DDBJ
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A; Reference number: $42669; MUID:85126934; PMID:6396087
A; Accession: $42669
A; Molecule type: mRNA
A; Residues: 101-393 <ARKII>
A; Residues: 101-393 <ARKII>
A; Cross-references: EMBL:X01405; NID:935215; PIDN:CAA25652.1; PID:9642241
B; Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.
A; Reference number: A22837; MUID:85230577; PMID:4006916
A; Accession: A22837; MUID:85230577; PMID:4006916
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A; Residues: 1-393 <LAM>
A; Residues: 1-393 <LAM>
A; Residues: 1-393 <LAM>
A; Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; PID
B; Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
Gene 70, 245-252, 1988
A; Title: A variation in the structure of the protein-coding region of the human p53 gene
A; Reference number: J70436; MUID:89108008; PMID:2905688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cellular tumor antigen p53 [validated] – human
N'Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppress
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C; Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C; Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C; Caccession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; B25397; S42695; I58834; I78850; I52681; S60153
R; Lamb, P.; Crawford, L.
Mol. Cell. Biol. 6, 1379-1385, 1986
A; Title: Characterization of the human p53 gene.
A; Reference number: A25224; MUID: 87064416; PMID: 2946935
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A; Residues: 1-71, Pv. 73-393 <2AK>
A; Residues: 1-71, Pv. 73-393 <2AK>
A; Cross-references: EMBL: X02469; EMBL: M60950; NID: g35209; PIDN: CAA26306.1; PID: g35210
B; Harlow, B.; Williamson, N.W.; Relaton, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A; Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular a
A; Reference number: A55060; MUID: 85267676; PMID: 3894933
                                                                                                                         ::| :: |:|| :: |:|| 340 RFKMFQELNEALELKDAQALKASEDSGAHSSYLKSKKGQSASRLKKLMI-----388
223 YEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTITLEDPSGNLLGRNSFEVRICACPG 282
                                                                                                                                                                                                                    371 TYEMLLKIKESLELMQYLPQHTIE-----TYRQQQQQQHQHLLQKHLLSACFRNELVEP 424
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A; Residues: 1-393 <CHU>
A; Residues: 1-393 <CHU>
A; Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
B; Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, EMBO J. 3, 3257-3262, 1984
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A; Residues: 1-71, 73-393 <BUC2>
A; Cross-references: EMBL: M22898; NID: g189474; PIDN: AAA59988 1; PID: g189476
A; Note: this 72-Pro allele was found in both normal and malignant cell lines
R; Chumakov. P. M.; Almazov. V. P.; Jenkins, J. R.
Submitted to the EMBL Data Library, August 1990
A; Reference number: $40773
                                                                        RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRE
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KREGP 393
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A;Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237; R;Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
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A; Cross-references: GB:X01237; GB:K01700; NID:953575
A; Cross-references: GB:X01237; GB:K01700; NID:953575
A; Arait, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
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A; Title: Immunologically distinct p53 molecules generated by alternative splicing. A; Reference number: S38822; MUID:87064640; PMID:3023970
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
A;Reference number: A22739; MUID:85027173; PMID:6092064
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A;Accession: S06336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Zakut-Houri, R; Oren, M; Bienz, B.; Lavie, V.; Hazum, S.; Givol, D. Nature 306, 594-597, 1983.
A;Title: A single gene and a pseudogene for the cellular tumour antigen p53. A;Reference number: A02684; MUID:84068204; PMID:6646235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                               RAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQS
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A;Accession: S38823
                                                                                    47;
              Length 393;
                                                                                    Indels
           Score 717.5; DB 1;
Pred. No. 8.4e-48;
); Mismatches 116;
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30.1%; Scor
41.2%; Pre-
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                                                                                 Conservative
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A; Residues: 1-390 <ARA1>
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              Query Match
Best Local S
Matches 156
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A; Retaus: translated from GB/EMBL/DDBJ
A; Residues: 1-213, 70, 255-393 < F11
A; Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 1991
R; Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A; Title: An Alu polymorphism intragenic to the TP53 gene.
A; Reference number: 138093; WUID:92107726; PMID:1762941
A; Reference number: 138093
A; Status: translated from GB/EMBL/DDBJ
A; Realdues: 1-393 < FUY
A; Residues: 1-393 < FUY
A; Residues: 1-393 < FUY
A; Cross-references: EMBL:X54156; NID:935213; FIDN:CAA38095.1; FID:q35214
R; Yamada, Y; Yoshida, T: Hayashi, K; Sekiya, T: Yokota, J: Hirohashi, S.; Nakatani, Cancer Res. 51, 5800-5805, 1991
A; Title: p53 qene mutations in gastric cancer metastases and in gastric cancer cell line
A; Reference number: A44905; MUID:92034678; PMID:1933850
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule types: 327-331, 'DGTSPQKENC' CHO>
A;Rosidues: 327-331, 'DGTSPQKENC' CHO>
A;Cross-references: GB:S66666; NID:9436292; PIDN:AAB28601.1; PID:9436293
A;Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymp
A;Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymp
Mol. Gen. Genet. 249, 425-431, 1995
A;Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragme
A;Reference number: S60151; MUID:96133682; PMID:8552047
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A; Molecule type: DNA
A; Motes: 246-247, W, 249-250 (YAM>
A; Cross-references: GB:S63157; NID:9237829; PIDN:AAB20140.1; PID:9237830
A; Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIP:63158)
A; Note: mutation from a liver metastasis of a gastric cancer
B; Hensel, C.H.; Xiang, N.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 6, 1067-1071, 1991
A; Title: Use of the single strand conformation polymorphism technique and PCR to detect
A; Reference number: IS8354; MUID:91296386; PMID:1648702
A; Accession: I58354
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residuas: 244-247, W', 249-252 (HENI)>
A; Accession: I78850
A; Accession: I78850
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A;Molecule type: DNA
B;Dang, C.V.: Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A;Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myb, N-myc, p53, HSP70,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Title: Alternative spliting of the p53 tumor suppressor gene in the Molt-4 T-lymphobla
A;Reference number: 152681; MUID:94036762; PMID:8221626
                                                                                                          A; Accession: 138090
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A; Cross-references: EMBL: X60018; NID: 9506,448; PIDN: CAA42633.1; PID: 950644$
A; Accession: 138091
A; Molecule type: mRNA
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-212, 'Q', 214-393 <F10>
A; Cross-references: EMBL: X60019; NID: 9506450; PIDN: CAA42634.1; PID: 9506451
A; Accession: 138092
                                            Residues: 1-247,'O',249-393 <F08>
Cross-references: EMBL:X60017; NID:9506446; PIDN:CAA42632.1; PID:9506447
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A;Molecule type: DNA
A;Residues: 274-277, S',279-282 <HEN2>
A;Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1; PID:g232816
R;Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
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Cydrosesion: S06594
R; Rigaudy, P.; Eckhart, W.
Nuclect Acids Res. 17, 8375, 1989
R; Rigaudy, P.; Eckhart, W.
Nuclect Acids Res. 17, 8375, 1989
R; Rigaudy, P.; Eckhart, W.
Nuclect Acids Res. 17, 8375, 1989
R; Rigaudy, P.; Eckhart, W.
Nuclectid sequence of a CDNA encoding the monkey cellular phosphoprotein p5 A; Reference number: S06594; MUID:90045967; PMID:2530498
B; Reference number: S06594
B; MUID:90045967; PMID:2530498
B; Residues: 1-393 ARIG>
B; Residues: 1-393 ARIG>
B; Residues: 1-393 ARIG>
B; Residues: EMBL:X16384; NID:922795; PIDN:CAA34420.1; PID:922796
B; Residues: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho F; 176,179,238,242/Binding site: zinc (Cys. His, Cys. Cys) #status predicted
F; 392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: JC6176
A;Molecule type: mRNA
A,Residues: 1-393 <LEE>
A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230
A;Cross-references: GB:U50395; NID:g1842229; TIDN:AAC53040.1; PID:g1842230
C;Comment: This protein is a multimer, it plays the central role in a complex DNA iption, and recombination by protein/protein interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDELLYLP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
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C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C;Accession: JC6176
                                                                                                                                                                           cellular tumor antigen p53 - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 QYTNLGLINSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSP----SPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 ------LTEDPGPDEAPRMSEAAPH--MAPTP-AAPTPAAPAPAPSWPLSSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 RAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 VLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 LSQETFSDLWKLLPE-----DLA--OW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
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626e 164, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster
A;Reference number: JC6176; WUID:97183659; PMID:9031625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.0%; Score 714.5; DB 1; 41.2%; Pred. No. 1.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||| :||| 332 IRGRERFEMFRELNEALEL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 VRGRETYEMLLKIKESLEL 384
| :|: :|
371 GQSTSRHKKTMVK 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S:
Matches 156,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
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                                                                                                                                                                                                                                                                                                                                             A;Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the A;Reference number: 148703; MUID:84272240; PMID:6379601
A;Reference number: 148703; MUID:84272240; PMID:6379601
A;Accession: 148703
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-47, RY, 49-78, QWY, 82-390 CRES>
A;Residues: 1-47, RY, 49-78, QWY, 82-390 CRES>
A;Cross-references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
C;Comment: This DNA-binding protein plays an essential role in the regulation of cell dicycomment: The tetramer association region may exhibit a beta-turn, beta-sheet, beta-tur C;Superfamily: cellular tumor antigen psi C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein; F:1-44/Domain: transcription activation #status predicted cTRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted 173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted 312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted 389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEG 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 RDGQVLGRRCFEARICACPGRDRRADEDSIRRQQVSDSTKNGDGTKRPFRQNTHGIQMTS 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                              A; Cross-references: EMBL.M13873
R; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter,
submitted to the EMBL Data Library, July 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SQSTQTNEF-LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                                                                                                                                                                 A; Accession: S40014
A; Molecule type: mRNA
A; Molecule type: 1-167, G',169-390 <ARA3>
A; Residues: 1-167, G',169-390 <ARA3>
A; Cross-references: EMBL: H13873; NID: 9200200; PIDN: AAA39882.1; PID: 9200201
R; Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOSDISLELPLSQETFSGLWKLL-------ILPSPHC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.3%; Pred. No. 1.3e-47;
ive 62; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;16-26/Region: conserved region I
F;99-289/Domain: DNA-binding core #status predicted <DBC>
                     A; Residues: 1-167, 'G', 169-233, 'I', 235-390 <ARA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%; Score 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;233-248/Region: L3 loop
F;267-287/Region: conserved region V
F;313-319/Region: nuclear location signal
F;319-357/Region: tetramer association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;168-178/Region: conserved region III
F;231-252/Region: conserved region IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;114-139/Region: conserved region II
F;160-192/Region: L2 loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 ООООООНОНЬТОК 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 166; Conservative
                                                                                                                                               A; Reference number: S40014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;108-121/Region: L1 loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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^O	71 OYTNIGILLNSMDOOJONGSSSTSPYNTDHAONSVTAPSPYAOPSSTFDAL-SPSPA 125	A: Experimental source: strain 129 SVI
á		C;Genetics:
a a	VANWLNEUFEEGLKVPAAFAPEA-PAFAAPALAAFATISWP	A;Map position: 9F1 A;Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
ογ	126IPSNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP 181	A; Note: basson
qq	90 LSSSVPSQKTYHGNYGFRLGFLHSGTAKSVTCTYSPCLNKLFCQLAKTCPVQLWVDSTPP 149	A; Description: may be involved in cytomatrix organization at the site of neurotransmi
Qy	182 QGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPI 241	A;Note: component of the presynaptic cytoskeleton C;Keywords: coiled coil; zinc finger
qa	: : :	Ouerv Match 4.8%: Score 114.5: DB 2: Length 3942:
à	TODOCUT THUST THE TEST OF THE PROPERTY TURBER TO THE TEST OF THE PROPERTY TO T	Similarity 21.2%; Pred. No. 9.4;
Š t	GONGS DAY LEFF OVER 11 VIII	Matches 113; Conservative of; Mismatches 190; indeis 109; Gaps
e e	AFRIDAVAVELEPPEAGODOLTIBINIMONDOCMGGMNKKFILIILLEDDOGNLLGKNAF	MSGSTQTNEFLSFEVFQHIMDFLEGFICSVQFIDLNFVDEFSED
δŏ	EARICACPGRDRRADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDEL	LGQGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDHRYGPRGDAVGFQEASLAQ
gg	268 EVRVCACPGRDRRTEEENFRKKGEPCPELPPGSSKRALPTTTTDSSPQTKKRPLDGEY 325	QY 45 -GATUKIEISMDCIRMQDSDLSDPWWPQYTNLGLLNSMDQQ-1QNGSSSTSPYNTD 98
δλ	362 LYLPVRGRETYEMLLKIKESLEL 384	YGG
qo	326 FILKIRGRERFEMFRELNEALEL 348	QY 99 HAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSAT 152
	13	Db 2136 HGP-GLSAPQGLAPLRSGLLGNPTYPEGQPSPGNLAQYGPAASQATAVRQLLPSTAT 2191
146226 cellula	r tumor antigen p53 - dog (fragment)	Qy 153WTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAMPVYKKAEHVTEVVK 203
C; Specia	es: Canis lupus familiaris (dog)	PMV
C; Acces	21 feb 123/ #sequence_revision 21 feb-139/ #text_change 03-may-2000.	Qy 204 RCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE-PPQVG 257
R;Devil	ee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C. cor Res. 14, 2039-2046, 1994	
A, Title	: The canine p53 gene is subject to somatic mutations in thypoid carcinoma.	
A; Refer A; Access	ence number: 146226; MUID:95150524; PMID:7847847 sion: 146226	QY 258 TEFTTVLXNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPG 310
A; Status	A; Status: preliminary; translated from GB/EMBL/DDBJ	Db 2288 KPAATKASGAGGPPRPELPAGVAREEPFSTTAPAVIKEAVAPAPGPAPAPPP 2340
A; Residu	uses: 1-77 See: 1-77 	QY 311RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQ 347
C; Genet.	Treferences: GB:LZ/03U; NID:g3U8434; FIDN:AAC3/3Z/.1; FID:g3U8435	Db 2341 GQKPAGEAAAGSGSGVLSRPASEKEEASQEDRQRKQQE
A; Gene: p A; Introns	p53 nns: 24/1; 61/3	LIKIKESLELMOYLPOHTIET
C; Super	Superfamily: cellular tumor antigen p53	: : : : : : : : : : :
Query Rest 1	Query Match 10.9%; Score 259.5; DB 2; Length 77;	200 UNGUENDIN PEDENDIN DINGEBERENEN PENKUNNEBERKEN VENKEBERENEN VENKUNNEN 2000 OFF UNIVERSITEER PENKUNNER VERBERENEN PENKUNNER VERBERENEN VENKUNNER VERBERENEN VERKUNNER VERBERENEN VERKUNNER VERBERENEN VERKUNNER VERBERENEN VERKUNNER VERBERENEN VERKUNNER VERKUNNER VERBERENEN VERKUNNER VERBERENEN VERKUNNER VERKUNNER VERBERENEN VERKUNNER
Matches	47; Conservative 16; Mismatches	:
QY	194 KAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP 253	DD 2437 -QQQEERQAQFALQREQLAQQRLQLEQIQQLQQQQQQQLQLEQRQRQRQRPFP 2486
qa	: : :	RESULT 15
ò		T32008
3 1	: :: : :	
qq	60 PEVGFDYTTIHYNYMCNS 77	C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C:Accession: T32008
RESULT 14	14	R;Davidson, S.; Wohldmann, P.; Mullen, G. submitted to the EMBL Data Library, July 1997
T42730		A. Description: The sequence of C. elegans cosmid K10G6.
C; Specie	Bassoon procein - mouse C:Species: Mus musculus (house mouse)	A; Reference number: Z21111 A; Accession: 173008
C; Access	ir Jan 2000 sequence revision ir Jan 2000 #text_change zi-Jur-2000 sion: T42730	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
R;Dieck J. Cell A;Title	R;Dleck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998	A; Residues: 1-1819 < CDAV> A; Cossa references: EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESP:K10G6.3 A; Experimental source: strain Bristol N2; clone K10G6
A;Refero A;Accest A:Status		C;Genetics: A;Gene CESP:KIOG6.3 A;Man noct+10n. 2
A: Resid	A; Molecule type: DNA A; Residues: 1.342 < OTE>	
A; Cross	references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810	Query Match 4.7%; Score 111.5; DB 2; Length 1819;

Search completed: August 7, 2003, 09:53:26 Job time: 18:1241 secs OTASU) NNA JE BLANK (USPTO)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 7, 2003, 09:32:13; Search time 7.94483 Seconds (without alignments) 2651.784 Million cell updates/sec Run on:

US-09-538-106-15 2383 1 MSQSTQTNEFLSPEVFQHIW......PKQSDVFFRHSKPPNRSVXP 448 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	hom	Q9xsk8 cercopithec	P25035 oncorhynchu	_	P79734 brachydanio	093379 ictalurus p	P07193 xenopus lae	tetrao	P41685 felis silve	sns sci	P10360 gallus gall	canis	P79820 oryzias lat		036006 marmota mon	P10361 rattus norv	_	O9ttal tupaia glis	_		012946 platichthys		P56423 macaca fasc		P13481 cercopithec					-	~	-	snnbə (
SUMMARIES		αī	P73_HUMAN	P73_CERAE	P53_ONCMY	P53_BARBU	P53_BRARE	P53_ICTPU	P53_XENLA	- 1	P53_FELCA	P53_PIG	P53_CHICK	P53_CANFA	P53_ORYLA	P53_BOVIN	P53_MARMO	P53_RAT	- 1	P53_TUPGB	P53_SHEEP	P53_MESAU	P53_PLAFE	P53_HUMAN	P53_MACFA	P53_MOUSE	P53_CERAE	P53_MACMU	P53_XIPHE	- 1	- 1	P53_RABIT		P53_HORSE	P53_EQUAS
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Q9y6v0 homo sapien Q05192 drosophila	P40872 bacillus su P23468 homo sapien	Q8bgt6 mus musculu	000409 homo sapien	P49415 drosophila	Q9jks6 rattus norv	P20134 saccharomyc	P22082 saccharomyc	Q24167 drosophila	Q9bvv6 homo sapien
PCLO_HUMAN FTFB_DROME	PKSM_BACSU PTPD_HUMAN	MI13_MOUSE	FXN3_HUMAN	SDC_DROME	PCLO_RAT	SFL1_YEAST	SNF2_YEAST	SIMA_DROME	Y586_HUMAN
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117.5	109	106.5	106	105.5	105.5	105	104.5	103.5	103
34 35	36	38	39	40	41	42	43	44	4 2

ALIGNMENTS

ALLUMENIS	P73_HUMAN ID P73_HUMAN STANDARD; PRT; 636 AA.	16-0CT-2001 (Re]	15-SEP-2003 (Rel. Tumor protein p73	protein). TP73 OR P73.	Homo sapiens (Human). Eukaryota; Metazoa; Chordata;	<pre>Mammalia; Eutheria; Primates; NCBI_TaxID=9606;</pre>	RC TISSUE=Colon; by MEDIIND=01433000, pubMcd=0389750.	Kaghad M., Bonnet H., Yang A., Creancier L., Biscan JC.,		RT frequently deleted in neuroblastoma and other human cancers."; RT. Cell 90.809-819/1907)		RP SEQUENCE FROM N.A. (ISOFORM ALPHA). DY MEDITNE-00280200: DibMed=10162363.	Harris C.C.;	RT "Mutational analysis of p/3 and p53 in human cancer cell lines."; RT. Oncodene 18:3415-3421/1999:	[3]	ے ج	Jenkins R., Smith D.I., Liu W.;		оше		RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).		Annicchiarico-Petruzzelli M., Levrero M., N.	RI "IWO new p/3 splice variants, gamma and delta, with different pm transcrintional activity ".	-	RN [5]	RX MEDLINE=99310938; PubMed=10381648;		
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AF079089; AF079090; A
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     DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER, APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO PS3. HEMIZYGOSITY IS OBSERVED IN NEUROBLASTOMA AND OLIGONERORROGILOMA. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOIG-015350-7; Sequence-VSP_006538;
ISOIG-015350-7; Sequence-VSP_006538;
TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
INDUCTION: NOT INDUCED BY DNA DAMAGE.
DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
TO THE ABL TYROSINE KINASE SH3 DOMAIN.
                                                                                   MEDLINE-99318135; PubMed-10391251;
Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
Kharbanda S., Weichselbaum R., Kufe D.;
"p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
to DNA damage."
Nature 399:814-817(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN.

SUBBRIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABLIVED TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA SUBCELLULAR LOCATION: Nuclear.

ALTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORM DELTA SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=015350-3; Sequence=VSP_006540, VSP_006541; Note=The splicing of exon 11 results in a frameshift from the original reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note-The splicing of exon 11 results in a frameshift from the original reading frame. The splicing of exon 13 reverts the reading frame to the sequence of isoform Alpha;
                                                                                                                                                                                                                                                                                                      MEDLINE-99380160; PubMed=10449409;
Chi S.W., APROAN, ALTOWSMITH C.H.;
Chi S.W., APROAN, ALTOWSMITH C.H.;
Chi S.W., APROAN, ALTOWSMITH C.H.;
ESDIUTION STRUCTURE of a CONSERVED C-terminal domain of p73 with structural homology to the SAM domain.";
EMBO J. 18:4438-4445(1999).
-I- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
WHEN OVERRERODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
                                                                                                                                                                                       Ή.
                                                                                                                                                                                  Yuan Z. M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu
Kharbanda S., Weichselbaum R., Kufe D.;
Nature 400:792-792(1999).
                                       Thomas D.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=015350-4; Sequence=VSP_006542, VSP_006543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Epsilon;
IsoId=015350-5; Sequence=VSP_006544, VSP_006545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=7;
                                                                          PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Beta;
IsoId=O15350-2; Sequence=VSP_006539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=015350-1; Sequence=Displayed;
                                                                                                                                                                                                                                                         Kaelin W.G. Jr.,
"The emerging p53 gene family.";
J. Natl. Cancer Inst. 91:594-598(1999).
Cell Death Differ. 6:389-390(1999).
                           SEQUENCE FROM N.A. (ISOFORM KAPPA).
                                                                                                                                                                                                                                               MEDLINE=99217940; PubMed=10203277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Kappa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
CYRMITWREADDLKQCHSYSTAQCLRSSNAATISIGGSGE
LQRQRVMEAVHFRYRHTITPNRGCPGGGDEWADFEPDLP
DCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSACTIVATION (BY SIMILARITY).
ASP/GID-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MEDIAPES OLIGOMERIZATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY ABL) (IN ISOFORM
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GO; 60:0003700; F:transcription factor activity; TAS.
GO; GO:0000870; P:transcription of apoptosis by DNA damage; TAS.
GO; GO:0006298; P:mismatch repair; TAS.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00970; P53.
Pfam; PF00956; SAM; 1.
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DNA-BINDING (POTENTIAL)
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                     EMBL; Y11416; CAA72220.1; -.
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AF077616; AAC61887.1;
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AF077618; AAC61887.1;
AF077619; AAC61887.1;
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                                                                                                                                                                                                                Y11416; CAA72219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE. WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
                                                                                                                                                    ----EIS
                                                                  MDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP
                                                                                                            SSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQ
                                                                                                                                                                                                                                 AQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDG
                                                                                                                                                                                                                                             QVLGRRCFEARICACPGRDRKADEDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--T
                                                                                                                                                                                                                                                                                        SIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQ--QQHQHL
                                                                                                                                                                                                                                                                                                                                  343 GVKKRRHGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQQQLLQRPSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                       IKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSH
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                    1 MSQSTQTNEFLSPE---VFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKI-
                                                                                                                                                                                                                                                                                                                                                                                                 P73_CERAE STANDARD; PRT; 637 AA.
095XSR4, 09FS09.
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
protein p73 (p53-like transcription factor) (p53-related protein).
                               31;
         636;
         Length
                               84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caput D.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
        54.4%; Score 1297.5; DB 1;
61.4%; Pred. No. 8.7e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA)
                              47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=09XSK8-2; Sequence=VSP_006537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoId=Q9XSK8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
                              258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name-Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name-Beta;
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produced through a collaboration
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PROSITE; PS00048; P53; 1.

Transcription regulation; Activator; DNA-binding; Anti-oncogene;

Transcription regulation; Phosphorylation; Alternative splicing.
Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
VARSPLIC 495 637 SFLTGLGCPNCIEYETSQGLQSIXHLQNLFIEDLGALKIPE
OVENTIMEQUEDENGORDANAISTGGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 IKVSAPPPPGTAIRAMPVYKKABHVTDIVKRCPNHELGRDFNEGQSAPASHLIRVEGNNL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
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7CB200B919C9C70A CRC64;
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TP53.
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Pred. No. 1e-88;
48; Mismatches 8
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Last sequence update)
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Pfam; PF00536; SAM; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.48;
                                                                                                                                                                                                                                                                                                                    EMBL; Y11419; CAA72224.1; -. EMBL; Y11419; CAA72225.1; -. HSSP; O15350; ICOK.
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01-MAY-1992 (Rel. 22, Last
28-FEB-2003 (Rel. 41, Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002117; P53
InterPro; IPR001660; SAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDALS-PSPAIPS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
                                                                          de Fromentel C.C., Padkel F., Chapus A., Baney C., May P., Soussi T., Rainbow trout p53: cDNA cloning and blochemical characterization."; Gene 112:241-245(1992).

1- FONCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BCI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 GYDNF----MAEAPLQ-----VEFDPSLFEVSATEPAPQPSISTLDTGSPPTSTVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 NTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KMNLNLVAVQPPETE----SWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 MPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY SIMILARITY). 8422250765545A1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 396;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                           expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 847.5; DB 1
Pred. No. 1.1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                  SEQUENCE FROM N.A. MEDLINE=92210006; PubMed=1339362;
                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 LSQESFEDLW------
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M75145; AAA49605.1; -. PIR; JH0631; JH0631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325
369
303
395
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JH0631; JH0631
HSSP; P04637; lTUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                          NCBI_TaxID=8022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
DOMAIN
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DOMAIN
MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
84 QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 ELINDEYLPSSFDPNIFDNVLTEQPQPSTSP-----PTASVPVATDYPGEHGFKLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                              Barbus barbus (Barbel).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Barbus.
NCBI_TaxID-40830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein; Phosphorylation; Apoptosis.

1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.4%; Score 819.5; DB 1; Length 369; 51.2%; Pred. No. 1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBE2CF2CEA74C304 CRC64;
                                                                                         : | :||:| |||| | :|||| : :| : |||| : 327 IYTLQIRGKEKYEMLKKFNDSLELSELVPVADADKYRQK 365
                                                                                                                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
18-0CT-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.2e-53;
                                                              361 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ
                                                                                                                                                                                                                369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF071570; AAD34212.1; -. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS: PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41233 MW;
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Best Local Similarity 51.28
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298
342
276
368
369 AA;
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                                                                                                                                                                                                                P53_BARBU
                 267
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SEQUENCE
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                                                                                                                                                                                                                                         Q9W678;
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P53_BARBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 373
                                                                 262
                                                                                                                                 322
                                137
                                                                                                                                                                                                                              DQ---ETKTLDKIPSANKRSLTKDSTSSVPRPEGSKKAKLSGSSDEEIYTLQVRGKERYE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97344388; PubMed=9200835;
Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
"Zebrafish (Danio retaio) p53 tumor suppressor gene: cDNA sequence and
QQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVV
                    KRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTT
                                                                                 VLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRK
                                                                                                                                                QQVSDSTKNGD----GTKRPF-RQNTHGIQMTSIKKRR----SPDDELLYLPVRGRETYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BCI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Buteleostomi;
Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Winge P.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                 P53_BRARE STANDARD; PRT; 373 AA. P79734; Q90440; Col.NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53). TP53 OR DRP53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Mar. Biol. Biotechnol. 6:88-97(1997)
                                                                                                                                                                                                                                                               374 MLLKIKESLELMQYLPQHTIETYRQQ 399
                                                                                                                                                                                                                                                                                  ZFIN; ZDB-GENE-990415-270; tp53.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 140-212 FROM N.A.
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P04637; 1TUP.
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143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR 291
                                                                                                                                                                                                                                                                                                                                                                                                            Luft J.C., Bengten E., Clean L.W., Miller N.W., Wilson M.R.;
Luft J.C., Bengten E., Clean L.W., Miller N.W., Wilson M.R.;
"Identification and characterization of the tumor suppressor p53 in channel catfish (Irctalurus punctatus).";
Comp. Biochem. Physiol. 1208:675-682(1998).

-i- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGQVLGRRCFEARICACPGRDRKADEDSIRK-QQVSDSTKNGDGTKRPFRQNTHGIQM--
                                                                                                                                                                                                                                                                                                                    112 QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
                                                                                                                                                                                                                                                                                                                                                                                        172 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                         BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --TSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ
                                                                                     Nuclear protein; Phosphorylation; Apoptosis.

1 31 TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                                                          PHOSPHORYLATION (BY SIMILARITY). AC7AB724FA6B61FF CRC64;
                                                                                                                                                                                                                                               33.8%; Score 805.5; DB 1; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Tumor suppressor p53)
                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                 1.3e - 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-EFB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p
                                                                                                                                          OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                      BY SIMILARIT
                                                                                                                                                                                                                                                                   Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-99071979; PubMed-9854815;
                                                                                                                                                                                                                                                                              42;
Pfam; PF00870; P53; 1.
PRINTS, PR00386; P53SUPPRESSR.
ProDom; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                            41899 MW;
                                                                                                                                                                                                                                                               53.9%;
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                       332
366
296
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                                                                                                                                                                                                            373 AA;
                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ictaluridae;
                                                                                                                                                                                                                                                                                 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P53_ICTPU
093379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                      DNA_BIND
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                   Sest Local
Matches 15
                                                                                                                                                                                             MOD_RES
                                                                                                                                          DOMAIN
                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 SDMLQPQSS--SSPPTSTVPVTSDYPGLLNFTLHFQESSGTKSVTCTYSPDLNKLFCQLA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQ 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQHQHL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPYAOPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 ASKKSKNSSSDDEIYTLQVRGKERYEFLKKINDGLELSDVVPPADQEKYRQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR
                                                                                                                                                                                                                                                                                                                                       BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSHORYLATION (BY SIMILARITY).
1B89CD98DB3289F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                    HSSP; rc.
InterPro; IPR00411.,
R PRINTS; PR00386; P53SUPPRESSR.
R PRINTS; PR00386; P53SUPPRESSR.
R Probom; P0002681; P53; 1.
DR PROSITE; P500348; P53; 1.
DR Anti-oncogene; DNN-binding; Transcription regulation; Activator; KW Anti-oncogene; DNN-binding; Transcription ACTIVATION (ACIDIC).
TOWAIN 1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
TOWAIN 1 268 BY SIMILARITY.
OLIGOMERIZATION.
OLIGOMERIZATION.
TOWAIN (REPRESSION OF DNA-BINDING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-88143684; PubMed-2830576;
Soussi T., de Fromentel C.C., Mechali M., May P., Kress M.;
"Cloning and characterization of a cDNA from Xenopus laevis coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 1; Length 376; 3.5e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 3.5e
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LLSKTCRKERDGAAGEPKR 362
                                                                                                                                      EMBL; AF074967; AAC26824.1; -. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                          41989 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         33.6%;
50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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P07193;
                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 DALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVM 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTF 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
T -> S (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                             2 SQSTQTNEFLSPEVFQHIWDFLEQPI----CSVQPIDLNFVDEPSEDGATNKIEISMDCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SSETGMDPPLSQETFEDLWSLLPDPLQTVTCRLDNLS-EFPDYP------LAADMT
                                                        Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.; "Overexpression of Wild-type p53 interferes with normal development in Xenopus laevis embryos."; Oncogene 9:109-120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein; Phosphorylation; Apoptosis.

DOMAIN 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CE1F3E58F020D74D CRC64;
for a protein homologous to human and murine p53."; Oncogene 1:71-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.6%; Score 777.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 VLQE------GLMGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.5e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55; Mismatches
                                       SEQUENCE FROM N.A. MEDLINE-94134403; PubMed=8302570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X05191; CAA28821.1; -.
EMBL; X77546; CAA54672.1; -.
EMBL; S68353; AAC60746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M36962; AAA49923.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.58;
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Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 42.5
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331
356
293
362
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71
296
363 AA;
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                            297
                                                                                                 242 RRCFEVRVCACPGRDRRTEEDNYTKKRGLKPSGK------RELAHPPSSEPPLPKKR 292
SPPPRGSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
"Evolutionary conservancy of p53 gene sequences in fish.";
"Evolutionary conservancy of p53 gene sequences in fish.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle. Fegulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                        RRCFEARICACPGRDRKADEDS-IRKOOVSDSTKNGDGTKRPFRONTH--GIOMTSIKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.

OLIGOMERIZATION.

BASIC (REPRESSION OF DNA-BINDING).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

ACCIOEE22F5F9CFD CRC64;
                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Taleosstei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Phosphorylation; Apoptosis.

1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                            R---SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 393
                                                                                                                                                                       293 LVVVDDDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV 334
                                                                                                                                                                                                                                                                                                                Cellular tumor antigen p53 (Tumor suppressor p53).
TP53 OR P53.
                                                                                                                                                                                                                                                                      16-0cr-2001 (Rel. 40, Created)
16-0cr-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                             367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                 Tetraodon miurus (Congo puffer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF071571; AAD34213.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
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PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002117; P53.
                                                                                                                                                                                                                                             STANDARD;
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342
288
366
367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=94908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P04637
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09W679;
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SEQUENCE
                                                                                  298
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249
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                                                                                                                                                                                                                                                                                                                                                         130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAM 189
                                                                                                                                                                                                                                                                                                                                                                                       145 AIYKKTEHVAEVVRRCPHHQ-----NEDSAEHRSHLIRMEGSERAQYFEHPHTKRQSVTV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS-----PDDELLY 363
                                                                                                                    20
                                                                                                                                                                                                                                                                                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                    11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                               42 AERQMNMMCNFMDSTFNEALFNLLP-------EPPSRDGANSSSPTVPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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J. Vet. Med. Sci. 55:801-805(1993).
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                              ----TIQTAALENEAWP
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y., Wateri T., Goitsuka R., Tsujimoto H., Hasegawa A.; "Cloning of feline p53 tumor-suppressor gene and its aberration in hematopoietic tumors."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 34-354 FROM N.A.
MEDLINE=94114699; PubMed=6286534;
Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T., Goitsuka O'Srien S.J., Tsujimoto H., Hasegawa A.;
"Molecular cloning and chromosomal mapping of feline p53 tumor
                                                          64;
   DB 1; Length 367;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
08-FBE-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
TP53 OR TRP53.
                                                          53; Mismatches 105;
32.6%; Score 776; DB 1
42.6%; Pred. No. 2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 LPVRGRETYEMLLKIKESLELMOYLPO 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Lymph node;
MEDLINE-94333960; PubMed-8056458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Int. J. Cancer 58:602-607(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Felis silvestris catus (Cat).
                                                          Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P53_FELCA
P41685;
      Query Match
                                 Best Local
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rP53 OR P53.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         .7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85
                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSFVPSQKTYPGAYGFHLGFLQSGTAKSVTCTYSPPDFNKLFCQLAKTCPVQLWVRSPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 FRHSVVVPYEPPEVGSDCTIHIYNFMCNSSCMGGMNRRPIITITLEDSNGKLLGRNSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VANWLDEA-----PDDASGMSAVPAPAAPAAT----PAPAISWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSQETFSELWNLLPE-----NNVLSSELSSAMNELPLSED-------
                                                                                                                                                                                                                                                                                                            BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
         SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                        Transcription regulation; Activator;
                                                                                                                                                                                                                                                                  Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                  Score 770; DB 1; Length 386; Pred. No. 6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                        58; Mismatches 103; Indels
 SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                    -> R (IN REF. 2).
D08B43BA1BC8EB78 CRC64;
                                             in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                  OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 AA.
                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 TLQIRGRERFEMFRELNEALEL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 YLPVRGRETYEMLLKIKESLEL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                      PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                              42692 MW;
                                                                                                                                                               EMBL; D26608; BAA05653.1; -. EMBL; D16460; BAA03927.1; -. HSSP; P04637; 10LG.
                                                                                                                                                                                                                                                       Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                    32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                               42.18;
                                                                                                                                                                                                InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                       385
285
386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                 318
361
304
                                                                                                                                                                                                                                                                            DOMAIN
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                       MOD_RES
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                       DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P53_PIG
Q9TUB2;
                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
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P53_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSRAIPSNT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 DYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
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                                                                                                                                                                                                                                                                               MEDLINE-99422034; PubMed-10490836;
Burr P.D., Argyle D.J., Reld S.W.J., Nasir L.;
"Nucleotide sequence of the porcine p53 cDNA, and the detection of
recombinant porcine p53 expressed in vitro with a variety of anti-p53
antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                     -----VINWLDENPDDASRVPAP-----PAATAPAPAAPAPATSWPL--SSFVPSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 LSQETFSDLWKLLPE------NALLSSELSLAAVNDLLLSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; Phosphorylation; Apoptosis. J
DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
DINA BIND 91 BY SIMILARITY.
DOMAIN 318 349 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY SIMILARITY).
A4C3D88E8DF55162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Mismatches 125; Indels
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                        16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.2%; Score 767; 38.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 2.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF098067; AAF04620.1; -. HSSP; P04637; 1C26.
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42862 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00870; P53; 1
                                                                                                                               Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
304
15
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                                                                                                                                                          272
VYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVP 250
                                                                     YEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLILVTLETRDGQVLGRRCFEARICACPG 310
                                                                                                                                                                                         RDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRE 370
                                                                                                                                                                                                               371 TYEMLLKIKESLELMQYLPQHTIETYRQ--QQQQQHQHLLQKHLLSACFRNELVEPRRET 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 16:11383-11383(1988).

Nucleic Acids Res. 16:11383-11383(1988).

- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2. SUBUNIT: Bidds DMA, as a homotetramer (By similarity).
                                                                                                                                          330 RFEMFRELNDALELKD-----KGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89083584; PubMed-3060861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X13057; CAA31456.1; -. PIR; S02193; S02193.
                                                                                                                                                                                                                                                                                                                                                                 PS-----RHKKP 376
                                                                                                                                                                                                                                                                                                                                PKQSDVFFRHSKP 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S02193; S0219:
HSSP; P04637; 1TUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPAFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P53_CHICK
P10360;
                                                                                                                                                                                                                                                                                                                                                               370
                94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 GRDRKIEBEBNFRK------RGGAGGVAKRAMSPPTEAPEPPK-KRVLNPDNEIFYLQVR 316
                                                                                                                                                                                                                                                                                            70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
                                                                                                                                                                                                                                                                                                                                                      130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRDRKADEDSIRKQQVSDSTKNGDG--TKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVR 367
                                                                                                                                                                                                                                    69
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Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
Watari T., Hasagawa A., Tsujimoto H.;
"Aberrations of p53 tumor suppressor gene in various spontaneous
tumors in the dog.";
                                                                                                                                                                                                                                                       9 LEPTEVFMDLWSMLPY---SMQQL----PLPEDHSNWQELS----PLEPSDPPPPPP
                                                                                                                                                                                                                                    11 LSP-EVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMW
                                                                                                                                                                                                                                                                                                                                                                                                                PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                146 AVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPAQHLIRVEGNPQARYHDDETTKRHSVVV
                                                                                                                                                                                                                                                                                                                         55 PPPLPL-----TPPRAAPSPVVPST
                                                                                                  BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
FC3700FCDF9195B6 CRC64;
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Veldhoen N., Milner J.;
Isolation of canine p53 cDNA and detailed characterization of the
full length canine p53 protein.";
Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                              Transcription regulation; Activator;
                                                                                                                                                                                                         55;
    Product: reverse...

PROGUE: PROGUAGE: P53: 1.

Anti-oncogene: DNA-binding; Transcription regulation; Activator
Anti-oncogene: DNA-binding; Transcription regulation; Activator
Nuclear protein; PhosphoryLation; Apoptosis.

TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                            DB 1; Length 367;
                                                                                                                                                                       32.1%; Score /04.0, 44.6%; Pred. No. 1.4e-49; tive 50; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                      BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98178696; PubMed-9519881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRETYEMLLKIKESLELMQ 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P53_CANFA STANDARD, CQ29537; Q9TV78; Created) 01-NOV-1997 (Rel. 35, Created)
                                                                                                                                              40169 MW;
                                                                                                                                                                                                         169; Conservative
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                      278
339
364
306
366
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347
292
366
367, AA;
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                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9615;
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                                                        DOMAIN
DNA_BIND
DOMAIN
DOMAIN
                                                                                                                 DOMAIN
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                190
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 KTYPGTYGFRLGFLHSGTAKSVTWTXSPLLNKLFCQLAKTCPVQLWVSSPPPPNTCVRAM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 POYTNIGLINSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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                                                            14 LSQETFSELWNLLPE------NNVLSSELCPAVDELLLPESVVNWLDEDSDDAPRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSD-PMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 P-----SSWPL----SSSVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALLZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                          -1- DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein; Phosphorylation; Apoptosis.

1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.6%; Score 753.5; DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
 to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEES -> MQEP (IN REF. 2).
L -> P (IN REF. 2).
761A718FDC93DA59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 le-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.
                                                    MEDLINE-95323915; PubMed-7600529;
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF060514; AAC16909.1; -.
EMBL; AB020761; BAA78379.1; -.
FMRT: S77819; AAB42022.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PRO0386; P53SUPPRESSR. Probom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 25-300 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S77819; AAB42022.1;
HSSP; P04637; 10LG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002117; P53.
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375
311
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Submitted (DEC-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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356
299
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DOMAIN
DOMAIN
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MOD_RES
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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148 AIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRNTFRHSVVV 206
                                                                                                                  369
                                                                                                                                          310 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;

"Isolation of CDNAs encoding the p53 tumor suppressor gene in the
"Isolation of CDNAs encoding the p53 tumor suppressor gene in the
Japanese Medaka (Oryzlas latipes).";

Submitted (MAX-1997) to the EMBL/GenBank/DDBJ databases.

-I FUNCTION: Acts as a tumor suppressor in many tumor types;

growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes regulared for this process. One of
the activated genes is an inhibitor of cyclin dependent kinases.

Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
MEDLINE-97305153; PubMed-9161419;
MEDLINE-97305153; PubMed-9161419;
"Chause M.K., Rhodes L.D., van Beneden R.J.;
"Cloning of the p53 tumor suppressor gene from the Japanese medaka (Oryzias laties) and evaluation of mutational hotspots in MNNG-exposed fish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryzlas latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53_ORYLA STANDARD; PRT; 352 AA. P79820; 09PSU7; 09PSU8; 01-NOV-1997 (Rel. 35, Created) 28-FFB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT THR-91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF003949; AAD01195.1; -. AF003950; AAD01196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U57306; AAC60146.1; -.
EMBL; AF003949; AAD01195.1; -
                                                                                                                                                                                                                                    324 ERYEMFRNLNEALEL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002117; P53.
                                                                                                                                                                                             370 ETYEMLLKIKESLEL
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Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                         256 VGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKA 315
                                                                                                                                                                                                                                                                                                            EHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQ 255
                                                                                                                                                                                                                                                                                                                                    DEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS------PDDELLYLPVRG 368
                                                                                                                                                                              22
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                                                                                                                                                                                                                                                                                                                                              FQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQYTNL
                                                                                                                                                                           14 FOELWETVSYP--PLETLSLPTVNEPTGSW-----VATGDMFLLDQDLS-----
                                                                                                                                                                                             76 GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGP
                                                                                                                                                                                                             ---GTFDDKI-----FDIP---IEPVPINEVNPPPTTVPVTTDYPGS
                                                                          NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                  Bos indicus (Zebu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F., Kettmann R., Burny A., Willems L.; ide sequence of the bovine P53 tumor-suppressor cDNA.";
                                                                                                                                            69;
                                                                  BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTEN
                                                                                                                             DB 1; Length 352;
                                                                                                                                              Indels
                                                                                                   MISSING (IN REF. 1).
196868A66351BFF5 CRC64;
                                                                                                                                             92;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53)
                                                                                                                                     3e-48;
                                                  BY SIMILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                386 AA
                                                                                                                                             54; Mismatches
                                                                                                                            31.3%; Score 746.5; 43.1%; Pred. No. 3e-
                                                                                            <u>+</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-Bovine; TISSUE-Liver;
MEDLINE-95352829; PubMed-7626789;
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RERYEFLKKINDGLELLE 329
                                                                                                                                                                                                                                                                                                                                                                    RETYEMLLKIKESLELMQ 386
                                                                                                            ¥Σ.
PR00386; P53SUPPRESSR
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SEQUENCE OF 13-386 FROM N.A.
                                                                                                    39753
                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine), and
        PD002681; P53; 1
PS00348; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                          331
350
295
351
91
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NCBI_TaxID=9913, 9915;
                                                         302
334
283
351
91
22
352 AA;
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
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Matches 163;
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Q29628;
                                                                                                   CONFLICT
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                PROSITE;
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Best Local (
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DOMAIN
DOMAIN
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SPECIES-Bovine; STRAIN-Holstein; TISSUE-Thymus;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 GAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                         Bishop R.R.P., Gobright E.E.I.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling as et of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BcI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFVPSQKTYPGNYGFRLGFLQSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWVDSPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
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                           Komori H., Ishiguro N., Horluchi M., Shinagawa M., Aida Y.;
"Predominant p53 mutations in enzootic bovine leukemic cell lines.";
Vet. Immunol. Immunopathol. 52:53-63(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBDUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELIGLAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
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1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
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OLIGOMERIZATION
OLIGOMERIZATION
NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.1%; Score 741.5; DB 1; Length 386; 38.4%; Pred. No. 7.9e-48;
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222473F28C548F31 CRC64;
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                                                                                                                                                                          STRAIN-Boran; TISSUE-Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in many types of cancer.
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MEDLINE=96401400; PubMed=8807776;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43255 MW;
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Pfam; PF00870; P53; 1.
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                                                                                                             [3]
SEQUENCE FROM N.A.
                                                                                                                                                                          SPECIES-B.indicus;
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**REDLINE-97376996; PubMed-9233767;

**REDLINE-97376996; PubMed-9233767;

**REDLINE-97376996; PubMed-9233767;

**Partial characterization of the woodchuck tumor suppressor, p53, and ts interaction with woodchuck hepatitis virus X antigen in hepatocarcinogenesis.";

**Oncogene 15.327-336(1997).

**Concogene 15.327-336(1997).

**Concoge
                                                                                               362 LYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH-QHLLQKHLLS-ACFRN 419
                                                                                                                                                                                                                                                                                            303 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL 361
                                                                                                                                                                                               243 GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 AA
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Pfam; PF00870; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                             420 ELVEPRRETP 429
                                                                                                                                                                                                                                                                                                                                                                                                          376 PML--KREGP 383
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NCBI_TaxID=9995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 SSSVPSQNTYPGVYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWVDSTPPP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 VRVCACPGRDRRTEEENFRKR-----GEPCPEPPPRSTKRALPNGTSSSPQPKKRPL 321
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                                                                                                                                                                                                                                                                                                                           11 LSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWP
                                                                                                                                                                                                                                                                                                                                                                                                       71 QYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                   39 PMDDL-LLSSED--VENWFDK----GPDEALQMSAAPARAPTPAASTLAAPSPATSWPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNT-----HGIQMTSIKKRRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACF
                                                                                                                                                                                                                                                                                                                                                                   -----ENNALSPVLSP
                                                     BY SIMILARITY.
OLIGOMERIZATION.
OLIGOMERIZATION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                  70; Gaps
Transcription regulation; Activator;
                 Phosphorylation; Apoptosis. 44 TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                             SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                          DB 1; Length 391;
                                                                                                                                                                                                                                                                                  68; Mismatches 130; Indels
                                                                                                                                                                                                 E1DE5DB84BA40182 CRC64;
                                                                                                                                                                                                                                          30.9%; Score 736; DB 1
38.0%; Pred. No. 2e-47;
                                                                                                                                                                                                                                                                                                                                                                 14 LSQETFSDLWNLLP------
                                                                                                                                                                                                   43468 MW;
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNELVEPRRETP 429
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RHKKIIFKREGP 388
                                                                                                                                                                                                                                                                                  164; Conservative
                                                         290
354
321
15
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                                                                                                                                                                                                   391 AA;
                   Nuclear protein;
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                                        DOMAIN
DNA_BIND
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                                                                            DOMAIN
DOMAIN
DOMAIN
MOD_RES
                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                MOD_RES
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Search completed: August 7, 2003, 09:47:26 Job time: 9.94483 secs

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August 7, 2003, 09:41:09; Search time 36.046 Seconds (without alignments) 3207.225 Million cell updates/sec
                                                                                                                                                                                                US-09-538-106-15
2383
1 MSGSTQTNEFLSPEVFQHIW......PRQSDVFFRHSKPPNRSVYP 448
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                            830525 segs, 258052604 residues
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                    Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

830525

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_plant:*
sp_rodent:*
sp_rodent:*
sp_virus:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	09h3d2 homo sapien	0991el rattus norv	099je0 rattus norv	088897 mus musculu	Q9nph7 homo sapien	OHIC	O9h3d3 homo sapien	homod	09h3d4 homo sapien	homo	099jd7 rattus norv	Q99jd8 rattus norv	Ogdwz0 mus musculu	099je3 rattus norv	Q9jjp6 rattus norv	088898 mus musculu
	ID	09н3D2	099JE1	O99JE0	088897	O9NPH7	Q9P1B7	09нзрз	075195	Q9H3D4	Q9UE10	Q99JD7	Q99JD8	09QWZ0	Q99JE3	Q9JJP6	088898
	DB	4	11	11	11	4	4	4	4	4	4	11	11	11	1	11	11
	Nuery Match Length DB	487	470	487	483	471	516	555	641	9	680	538	555	555	663	680	089
æ	Query Match	100.0	98.0	98.0	96.3	91.7	91.7	91.7	91.7	91.7	91.7	91.0	91.0	91.0	91.0	91.0	91.0
	Score	2383	2335	2335	2296	2185	2185	2185	2185	2185	2185	2169	2169	2169	2169	2169	2169
	Result No.		8	m	4	വ	9	7	80	6	10	11	12	13	14	15	16

075922 homo sapien Q99jd9 rattus norv	O88899 mus musculu	Q9plb5 homo sapien Q9plb5 homo sapien	homo	homo	ОШО	8 mus	O89097 mus musculu	Q99jd6 rattus norv	Q99je2 rattus norv	Q9up74 homo sapien	075080 homo sapien	Q9dec7 gallus gall	Q98sw0 xenopus lae	Q8jhz5 brachydanio	Q8jfe3 brachydanio	Q8jhz6 brachydanio		Q9h3p8 homo sapien	Q9w664 barbus barb	Q9jjp2 mus musculu	Q9jjp1 mus musculu	Q8nhw9 homo sapien	Q8tdy5 homo sapien		Q96kr0 homo sapien	Q9cu77 mus musculu
4 0	Π,	416 4 USF1B6 461 4 Q9P1B5	61 4 Q9UP26	4	4	11	11	61 11 Q99JD6	11	56 4 Q9UP74	4	582 13 Q9DEC7	65 13 Q98SW0	13	٦	13	84 11 Q8C826	4	13	11	11	426 4 Q8NHW9	4	4	232 4 Q96KRO	14 11 Q9CU77
84.4 82.8	m	76.1	3 76.1	.16.1	3 76.1		76.0	75.8	75.8	75.4		73.2	9.69		63.1	63.1	59.5	57.2	55.7	1304 54.7 6	1271.5 53.4 5	52.5	12,48.5 52.4 4	5 52.4	.7 51.1	1085.5 45.6 5
17	910	270	22	3	24	. 25	56	27	78	53	30	31	32	33 15	34 15	35 15	36	37	38 13	39	40 12	41 12	42 12	43 12	44	45 10

ALIGNMENTS

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SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE
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                                                                                     Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                470;
                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21363379; PubMed-11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution of novel KET/p63:
"Variants.";
FEBS Lett. 501:121-126(2001).
-1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1. SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AJ277448; CAC37100.1;
HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                        470 AA; 53399 MW; 96B7ED2FB30DD394 CRC64;
                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             099JE0 PRELIMINARY; PRT; 487 AA. 099JE0; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                             Ouery Match 98.0%; Score 2335; DB 11; Best Local Similarity 98.0%; Pred. No. 4.2e-198; Matches 439; Conservative 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
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InterPro; IPR002117; P53.
Pffam; PF00870; P53; I.
PRINTS; PR00386; P535UPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2002 (TrEMBLrel. 22,
                                                                           Rattus norvegicus (Rat)
                                                   TA1 KET gamma protein.
                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                              Nuclear protein
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expression of the p51 gene in human lung cancer."; :-79(1999).
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                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 100.0%; Score 2383; DB 4; Length 487; Best Local Similarity 100.0%; Pred. No. 2.5e-202; Matches 448; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                         487 AA; 55687 MW; 86CC865BDF2643DD CRC64;
                       470 AA
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PROSITE; PS00348; P53; 1.
Nuclear protein.
                                                                                                                                                           BAA32592.1
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Pfam; PF00870; P53; 1.
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Similarity
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NCBI_TaxID=10090;
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                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                              Gaps
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                                                                                               Bamberger C., Schmale H.;
"Identification and tissue distribution of novel KET/p63 splice
                                                                                                                                                                                                                                           Length 487;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                         A688F392F32B3039 CRC64;
                                                                                                                       FEES LECET. 501:121-126(2001).
-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AJ277449; CAC37101.1; -.
HSSP; P04637; 1YCS.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; P0002681; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
Last annotation update)
                                                                                                                                                                                                                                        Score 2335; DB 11;
Pred. No. 4.4e-198;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 AA.
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                                                                              STRAIN-Wistar; TISSUE-Tongue;
MEDLINE-21363378; PubMed-11470269;
                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                          487 AA; 55499 MW;
                                                                                                                                                                                                                                          98.08;
98.08;
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01-OCT-2002 (TrEMBLrel. 22,
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Best Local Similarity 98.09
Watches 439; Conservative
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01-NOV-1998 (TrEMBLrel. 01
01-NOV-1998 (TrEMBLrel. 02
01-OCT-2002 (TrEMBLrel. 27
TA*p63 gamma.
          TA2 KET gamma protein.
                                                                      SEQUENCE FROM N.A
                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                Nuclear protein.
SEQUENCE 487 ?
                                                                                                                  variants.";
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                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=98448095; PubMed=9774969;

A MEDLINE=98448095; PubMed=9774969;

Yang,A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.;

Tapis, a p53 homolog at 3q27-29, encodes multiple products with transactivating death-inducing, and dominant-negative activities.";

Mol. Cell 2:305-316(1998).

I SINGELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

I SINGELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

I SINGELLULAR AAC6299.1; -

REMBL; ARC73434; AAC62639.1; -

REMBL; ARC7434; AAC62639.1; -

REMBL; ARC75434; AAC62639.1; -

REMBL; PRO754134; AAC6299.1; -

REMBL; PRO754134; PS3.

REMBL; PRO0754134; PS3.
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 12, Last annotation update)
P51 isoform Tap63delta (P51 delta protein).
P61 mon sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.2e-194;
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96.9%;
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           SEQUENCE FROM N.A.
BEDILINE-20388515; PubMed=10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
Yokota J.;
                                 "Mutation and expression of the p51 gene in human lung cancer."; Neoplasia 1:71-79(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBLARIARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                16;
                                                                                                                                                                                  Score 2185; DB 4; Length 471;
Pred. No. 8e-185;
3; Mismatches 7; Indels 1
                                                                                                                                                                       471 AA; 52882 MW; 32EB39798FC1CE69 CRC64;
                                            516 AA.
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01-OCT-2000 (TrEMBLrel. 15, Created)
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                                                                                                                                                                                   91.78;
94.18;
                                                                                                                                                     ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1. Nuclear protein. SEQUENCE 471 AA; 52882
                                                                                                                                                                                 Query Match
Best Local Similarity 94.1
Matches 416; Conservative
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AC Q9P11
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                                         Homo sapiens (Human).
Usukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 516;
                                                                                                          SEQUENCE FROM N.A.
MEDILINE-20388515; Pubmed-10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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  Last sequence update)
Last annotation update)
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ilarity 94.1%; Pred. No. 9.1e-185;
Conservative 3; Mismatches 7;
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  15, 1
22, 1
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AAF43488.1;
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Pfam; PF00870; P53; 1.
01-OCT-2000 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel. P51 isoform TAp63beta.
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Best Local Similarity
Matches 416; Conserv
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SEQUENCE 516
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                                                                                              TISSUE-Skeletal muscle;
MEDLINE-9832475; PubMed-9662378;
MEDLINE-98324755; PubMed-9662378;
Osada M., Obba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
"Cloning and functional analysis of human p51, which structurally and functionally resembles p53.";
Nat. Med. 4:839-844(1998).
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I "Mutation and expression of the p51 gene in human lung cancer.";

I Neoplasia 1.71-79(1999).

C -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

REMBL: ABOLGON3: BAA22593.1;

REMBL: AF116756; AAF43487.1; JOINED.

DR EMBL: AF116759; AAF43487.1; JOINED.

DR EMBL: AF116759; AAF43487.1; JOINED.

DR EMBL: AF116759; AAF43487.1; JOINED.

DR EMBL: AF116761; AAF43487.1; JOINED.

DR EMBL: AF116761; AAF43487.1; JOINED.

DR EMBL: AF116763; AAF43487.1; JOINED.

DR EMBL: AF116764; AAF43487.1; JOINED.

DR EMBL: AF116765; AAF43487.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              641 AA; 72019 MW; 97AE61F66E63F618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 1.2e-184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 09, Last seque
01-NOCT-2002 (TrEMBLrel. 22, Last annof
P51 isoform TAP63ALPHA (P51B protein).
                                                                                                                                                                                                                                                                        450 -----QTSIQSPSSYGNSSPP 465
                                                                                                                                                                                                                              421 LVEPRRETPROSDVFFRHSKPP 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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al Similarity 94.1%;
416; Conservative
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EMBL; AF116767; AAF43487.1;
EMBL; AF116768; AAF43487.1;
HSSP; PO4637; 1YCS.
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Pfam; PF00870; P53; 1.
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Matches
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Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
Ip63, a p53 homolog at 3427-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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Last annotation update)
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EMBL; AF124539; AAG45608.1; --
EMBL; AF124539; AAG45608.1; --
EMBL; AF124539; AAG45608.1; JOINED.
EMBL; AF124532; AAG45608.1; JOINED.
EMBL; AF124532; AAG45608.1; JOINED.
EMBL; AF124533; AAG45608.1; JOINED.
EMBL; AF124534; AAG45608.1; JOINED.
EMBL; AF124535; AAG45608.1; JOINED.
EMBL; AF124536; AAG45608.1; JOINED.
EMBL; AF124537; AAG45608.1; --
EMBL; AF124508.1; --
EM
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Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; P0002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                     01-MAR-2001 (TrEMBLrel, 16, 01-MAR-2001 (TrEMBLrel, 16, 01-OCT-2002 (TrEMBLrel, 22, TA p63 beta,
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                                                                                                 PRELIMINARY;
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SEQUENCE 555 #
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Homo sapiens (Human)
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                                                                    SPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP 180
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                                                                                                                            MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ
                      DSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL
                                                                                                                PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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MEDILINE-98448095; PubMed-9774969;
WEDILINE-98484095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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A STRAUSDEPELYMPH;

S. STRAUSDEPER R.;

S. STRAUSDEPER R. STRAUSDED R. STRAUSDED GATADASSES.

C. -- SUBMILARITY: BELONGS TO THE P53 FAMILY.

DR. EMBL; AF124528; AAG45607.1; -- ONDED.

DR. EMBL; AF124529; AAG45607.1; JOINED.

DR. EMBL; AF124531; AAG45607.1; JOINED.

DR. EMBL; AF124532; AAG45607.1; JOINED.

DR. EMBL; AF124533; AAG45607.1; JOINED.

DR. EMBL; AF124533; AAG45607.1; JOINED.

DR. EMBL; AF124533; AAG45607.1; JOINED.

DR. EMBL; AF124535; AAG45607.1; JOINED.

DR. EMBL; AF124535; AAG45607.1; JOINED.

EMBL; AF124535; AAG45607.1; JOINED.

EMBL; AF124536; AAG45607.1; JOINED.

EMBL; AF124536; AAG45607.1; JOINED.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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p63).
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                                                                                                                                                                                                                                                                                                 421 LVEPRRETPKQSDVFFRHSKPP 442
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TISSUE=Skeletal muscle, and Keratinocytes;
MEDINE=99018225; PubMed=9799841;
Augustin M., Bamberger C., Paul D., Schmale H.;
"Cloning and chromosomal mapping of the human p53-related KET gene tc chromosome 3427 and its murine homolog Ket to mouse chromosome 16.";
Mamm. Genome 9:899-902(1998).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                           Length 680;
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                                                                                                                                                                                                                                                                                        Nuclear protein.
SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;
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Last sequence update)
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Pred. No. 1.3e-184;
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AF124538; AAG45607.1; JOINED.
AF075430; AAC62635.1; -.
BC039815; AAH39815.1; -.
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                                                                                      Genew, HGNC.15979; TP63.
InterPro: IPR002117; P53.
InterPro: IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
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Best Local Similarity 94.1%;
Matches 416; Conservative
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                      Gaps
                                                                                                                                                     16;
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                                                                                                                                Query Match 91.7%; Score 2185; DB 4; Length 680; Best Local Similarity 94.1%; Pred. No. 1.3e-184; Matches 416; Conservative 3; Mismatches 7; Indels 1
                                                                                                               680 AA; 76776 MW; 6548A6F2187D852E CRC64;
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Last sequence update)
Last annotation update)
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
      -i - SIMILARITY: BELONGS TO THE P93 FAMILY.
EMBL; Y1661; CAA76562.1; -
HSSP; P04637; IYCS.
INTERPO: IPR002117; P53.
INTERPO: IPR001660; SAM.
Pfam; PF00870; P53: 1.
PRINTS; PR00386; P53: 1.
SWART; SM00454; SAM; 1.
PR005TE; P800348; P53; 1.
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STRAIN-Wistar; TISSUE-Tongue;
MEDLINE-21363378; PubMed-11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution of variants.";
-1- SUBCELLULAR LOCATION: NUCLEAR (BY
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(TrEMBLrel. 17, L
(TrEMBLrel. 22, L
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01-OCT-2002 (TrEMBLrel
TAl KET beta protein.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Identification and tissue distribution of novel KET/p63 splice
                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                 538 AA; 60326 MW; 66D0CA19786BF21B CRC64;
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Last annotation update)
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Pred. No. 2.5e-183;
5; Mismatches 9;
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     P53 FAMILY
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MEDLINE-21363378; PubMed-11470269;
Bamberger C.; Schmale H.;
                                                                                     PRINTS; PRO0386; P553UPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1. Nuclear protein. SEQUENCE 538 AA; 60326 MW;
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ilarity 93.2%;
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01-JUN-2001.(TrEMBLrel. 17,
01-OCT-2002 (TrEMBLrel. 22,
TAZ KET beta protein.
-1- SIMILARITY: BELONGS TO 1
EMBL; AJZ77452; CAC37104.1;
HSSP; PO4637; 1YCS.
InterPro; IPRO02117; P53.
Pfam; PF00870; P53; 1.
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PRINTS; PR00386; P53SUPPRESSR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                65D8854E2387C74C CRC64;
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Last annotation update)
                                                              Score 2169; DB 11;
Pred. No. 2.6e-183;
5; Mismatches 9;
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01-WAY-2000 (TERMBLrel. 13, Last sequ
01-0CT-2002 (TERMBLrel. 22, Last anno
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      Pfam; PF00870; P53; 1.
PRINTS; PR00386; P535UPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; P500348; P53; 1.
Nuclear protein.
SEQUENCE 555 AA; 62426 MW; (
                                                555 AA; 62426 MW;
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93.2%;
InterPro; IPR002117; P53.
                                                                       Local Similarity 93.2
Hes 412; Conservative
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MGD; MGI:1330810; Trp63.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                               Indels
                                                                    059E034046EB8987 CRC64;
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Last annotation update)
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FAMILY.
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                                                                                                              91.0%; Score 2169; DB 11;
93.2%; Pred. No. 2.6e-183;
1ve 6; Mismatches 8;
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FEBS Lett. 501:121-126(2001).
FISS Lett. 501:121-126(2001).
FISS Lett. 501:121-126(2001).
FISS Lett. 501:121-126(2001).
FISS LOAD LOCATION: NUCLEAR (BY 1-5 IMPLARITY: BELONGS TO THE P53 FAARIS, P04637; 14C5.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfan; PF00370; P53, 1.
PRINTS; PR00386; P53SIPPRESSR.
ProDom; P0002681; P53; 1.
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STRAIN-Wistar; TISSUE-Tongue;
MEDLINE-21363378; PubMed-11470269;
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                                                                    555 AA; 62454 MW;
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                                                                                                           Query Match 91.0°
Best Local Similarity 93.2°
Matches 412; Conservative
ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1. Nuclear protein. SEQUENCE 555 AA; 62454
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Gaps

16;

Score 2169; DB 11; Length 663; Pred. No. 3.4e-183; 5; Mismatches 9; Indels 16

91.0%; 93.2%;

C953BBAC389D5B70 CRC64;

9 82

P63. Rattus norvegicus (Rat). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. TISSUE-Lingual epithelium;
MEDLINE-97460723; PubMed-9315105;
Schmale H., Bamberger C.;
An novel protein with strong homology to the tumor suppressor p53.";
Oncogene 15:1363-1367(1997). Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases. -!- SUBCELLULAR LOCATION: NUCLERR (BY. SIMILARITY). -!- SIMILARITY: BELONGS TO THE P53 FAMILY. EMBL: Y10258; CAB88216.1; -. Last sequence update)
Last annotation update) 680 AA Created) 01-0CT-2000 (TrEMBLrel, 15, 01-0CT-2000 (TrEMBLrel, 15, 01-0CT-2002 (TrEMBLrel, 22, TAZ KET alpha. SEQUENCE FROM N.A. TISSUE-Lingual epithelium; Schmale H.; PRELIMINARY; SEQUENCE FROM N.A. NCBI_TaxID=10116; DDT TDD DDT TD

InterPro; IPR002117; P53. InterPro; IPR001660; SAM.

240 220 PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279 300 399 LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNE 420 FEARICACPGRDRKADEDSIRKQOVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDE 360 9 66 40 MSQSTQTSEFLSPEVEQHIWDFLEQPICSVQPIDLNFVDEPSENGATNKIEISMDCIRMQ 241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRC 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ PQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP Gaps Length 680; 680 AA; 76760 MW; AC45DABB88F61400 CRC64; Score 2169; DB 11; Pred. No. 3.5e-183; 5; Mismatches 9; 421 LVEPRRETPKQSDVFFRHSKPP 442 Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom, PD002681; P53; 1.
SMART; SM0454; SAM; 1.
PROSITE; PS00348; P53; 1. 91.0%; 93.2%; Best Local Similarity 33.2 Matches 412; Conservative Nuclear protein. SEQUENCE 680 A 301 361 400 181 450 Query Match SO WE DIR οy g δ g g g ద ç g οy g ò ò à ò

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completed: August 7, 2003, 09:51:40 he: 38.046 secs time Search c (OTARU) **XNAJB 3DA**9 21HT

OM protein

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Sequence:

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Database

Result Š

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Human cell regulatory protein p63, isoform deltaNp63 alpha.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                      ABG95141
ABP61915
ABB74995
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ABB74993
AAY05958
AAY50998
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ABG95135
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97US-0062076
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(HARD ) HARVARD COLLEGE
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N-PSDB; AAX58575.
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Homo sapiens.
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AAY05956;
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Human oncogene p51
Human p63 protein
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lung cancer-
lung cancer
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1 MLYLENNAQTQFSEPQYTNL........FNFDMDARRNKQQRIKEEGE 586
                                                                                August 7, 2003, 09:31:28 ; Search time 40.4138 Seconds
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                      1107863 seqs, 158726573 residues
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Listing first 45 summaries
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ABG95140
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AAY1032
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Human cell regulat

Rat KET protein. Human p63 protein

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cell regulat protein #2 u Human oncogene p63 Human p63 protein

p51 protein

Human Нимар

regulat

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The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour withch demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron stacs for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position intron. The human p53 gene was localised to chromosomal position of gamma forms, while p63 members differing in the N-terminus are designated as deltaN and TA forms, where the deltaN form lacks the capsignated as deltaN and TA forms, where the deltaN form lacks the designated as deltaN and TA forms, where the deltaN form lacks the capsignated as deltaN and TA forms, where the deltaN form lacks the capsignated as deltaN and TA forms, where the deltaN form lacks the p63 isotype hu-deltaNp63 alpha. p63 was detected in a variety of human and mouse tissue. It demonstrate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. DeltaN isotopes of p63 may also be implicated in hammatopolesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 may also be implicated in hammatopolesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative processes, in detection and diagnosis, and in the production of transgenic animals.
New isolated p63 cell regulatory protein for, e.g. treatment of
                                                                                   Claim 23; Fig 12; 161pp; English.
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586 AA; Sequence

180 9 1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS ö Length 586; Indels 100.0%; Score 3104; DB 20; 100.0%; Pred. No. 9.8e-244; 0; Mismatches Conservative Local Similarity 586; 61 61 121 Query Match Matches g δ 셤 ò

LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR 300 YVEDPITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIUTLETRDGQV 181 181 241 9 ŏ g δ

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SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG 361 361

DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 421 421

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481 QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR 540

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ABG95140 standard; Protein; 586

(first entry) 04-DEC-2002

ABG95140;

Human oncogene p63 isoform deltaN p63 alpha.

protein 90; Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein isoform; heat shock protein isoform; heat shock protein; fish-90; rheumatoid arthritis; cancer; haematopoietic disorder; cell lymphona; B cell lymphona; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; MLL; solid tumour; papillary thyroid carcinoma; Paving's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.

Homo sapiens.

WO200269900-A2.

12-SEP-2002

01-MAR-2002; 2002WO-US06518.

01-MAR-2001; 2001US-272751P.

(CONF-) CONFORMA THERAPEUTICS CORP.

Fritz LC, Burrows FJ;

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WPI; 2002-698710/75. N-PSDB; ABS73332 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90

Disclosure; Page 346-348; 389pp; English.

or a disease characterised by a solid tumour such as papillary thyroid carcinoma. Ewing's sarcoma, melanoma, libosarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.

Sequence

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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein or cellular protein isoforms (II) dependent on heat shock protein flow or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cencerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein or cellular protein isoform in a patient heteroxygous for (II). The method is useful cortaining disease e.g. hematopoietic disorder such as Tor B cellular tymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, In and Sandarderised by a solid tumour such as papillary thyroid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein
                                                                                                                                             Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
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Pred. No. 2.1e-243;
0; Mismatches 1;
                                                                                                                                                                                                                                    Disclosure; Page 331-333; 389pp; English.
                                      CORP
                                    (CONF-) CONFORMA THERAPEUTICS
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01-MAR-2001; 2001US-272751P
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Matches 585; Conservative
                                                                                                         WPI; 2002-698710/75.
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SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ 360
                                                                                                                                                                                                                                                                                                                                       Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X, Kalos MD, Henderson RA;
Durham M, Fanger GR, Vedvick TS;
Cai F, Foy TM;
                                               SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHHLQKQTSIQ
                                                                                                                                                                                                                                SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                               LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                          GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
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', Fanger N, Retter MW, Dur
Watanabe Y, Peckham DW, Ca
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07-MAY-2001; 2001US-0850716.
28-JUN-2001; 2001US-0897778.
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N-PSDB; ABQ92432.
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28-JUN-2001;
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McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-0CT-2002
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                       This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient cells expressing P2 and then administered to the patient to inhibit
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                                                                                                                                                                                                                                          Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic; vaccine; detection.
            QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
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Pred. No. 2.4e-242;
1; Mismatches 2;
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                                                                                                                                              AA.
                                                                                                                                            AAB11357 standard; Protein; 586
                                                                                                                                                                                                                                                                                                                                                                      99US-0285479.
99US-0466396.
99US-0476496.
2000US-0480884.
                                                                                                                                                                                                                   Human p63 protein isoform #1.
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11 Similarity 99.5%;
583; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fan L;
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10-JAN-2000;
22-FEB-2000;
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17-DEC-1999;
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McNeill
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                  The present invention describes isolated human lung carcinoma polynecleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide and comparing the macunt of polynucleotide that hybridises to the oligonucleotide and presence of a cancer in the patient. (I) and (II) are useful in presence of a cancer in the patient. (I) and (II) are useful in the presence or absence of a cancer such as lung cancer.

Comparing the presence or absence of a cancer such as lung cancer.

ABQ92145 to ABQ92486 and ABP61986 to ABP61992 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                            99.5%; Score 3087; DB 23; 99.5%; Pred. No. 2.4e-242; ive 1; Mismatches 2;
Example 2; Page 326-328; 381pp; English.
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583; Conserv
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                                                                                                                                                                                                                                         Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                         Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes human lung tumour proteins. Human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIRNGSSSTSPYNTDHAQNSVTAPSPYAQPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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NO:338
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protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAW, Li SX, Kalos MD,
Retter MW, Marnerakis M,
Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 3087; DB 23;
Pred. No. 2.4e-242;
; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer or stimulating an immune response
  p53 homologue isoform, p63 (L530S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 319-320; 374pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotides encoding lung
                                                                                                                                                                                                                                                                                            2000US-0630940
2000US-0643597
2000US-0662786
2000US-0685696
2000US-0735705
2001US-0850716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW,
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99.5%;
                                                                                                                                                                                                                                  28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                                                          2000US-0606421
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Best Local Similarity 99.5
Matches 583; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fanger N,
Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-090513/12.
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                                                             immune response
                                                                                                                                               WO200200174-A2.
                                                                                                                                                                                                                                                                                                                                                         09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                02-AUG-2000;
21-AUG-2000;
                                                                                                                                                                                                                                                                          28-JUN-2000;
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                                                      61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                                                     SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                  VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAO
                                                                                                                                                                              DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                     QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
  MLY LENNAQTQF SEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                  YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
                                                                                                                                                                                                                                                                          SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQHQHLLQKQTSIQ
                                                                                                                                                                                                                                                                                                                              SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTT1PDGMGAN1PMMGTHMPMAG
                                                                                                                                                                                                                                                                                                                                                                                               DMNGLSPTOALPPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTOGLFTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment; human; tumor; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GERVIDAVRFTLRQTISFPRDEWINDFNFDMDARRNKQORIKEEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human lung cancer-associated protein L530S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
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99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lung cancer; therapy; vaccine; detection.
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30-DEC-1999;
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                                                                                              480
                                                                                                                         480
                                                                                                                                                   540
                                                                                                                                                                cancer. The polypeptides and monoclonal antibodies specific for the polypeptides can also be used to inhibit the development of lung cancer. Agents which bind the polypeptides can be used for detecting lung cancer and for monitoring the progression of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated lung tumor polynucleotides, used to develop products for the treatment, prevention and monitoring the progression of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides isolated human lung tumor nucleic acids and polypeptides. The polypeptides can be used for the treatment of lung cancer. The polypeptides and polynucleotides can be used to stimulate cells or antigen presenting cells for use in the treatment of lung
DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                                                                   QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                      GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                                                                                                                                                                                                                                                                          tumor; lung cancer; T cell stimulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 3080; DB 20;
Pred. No. 8.8e-242;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 130-131; 148pp; English.
                                                                                                                                                                                                                                                                                                   Ā
                                                                                                                                                                                                                                                                                                  AAY41032 standard; protein; 586
                                                                                                                                                                                                                                                                                                                                                                               Human lung tumor antigen L503S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.2%; (stillarity 99.3%; ) Conservative 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0040984.
98US-0123912.
98US-0123933.
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es 582; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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Homo sapiens W09947674-A2

Human;

07-DEC-1999

AAY41032;

AAY41032 RESULT

17-MAR-1999;

23-SEP-1999

18-MAR-1998; 27-JUL-1998;

27-JUL-1998;

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Sequence

Query Match

Best Loca Matches

18-MAR-1998;

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07-0CT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                    TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                                                                                                                                                                                       SPDDELLYLPVRGRETYEMLLKIKESLELMÖYLPQHTIETYRQQQQQQHQHLLQKQTSIQ 360
                                                                              This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have eytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting calls expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                        TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR 300
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                     Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                                                                                                                                                                                                                      Indels
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Pred. No. 8.8e-242;
2; Mismatches 2;
                                                            Claim 3; Page 163-164; 261pp; English
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                                                                                                                                                                                                                               99.2%;
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es 582; Conservative
                                                                                                                                                                                         development of cancer.
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                                        in a patient -
                    Isolated
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ABP61869

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The present invention describes isolated human lung carcinoma polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide and oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in presence of a cancer in the patient. (I) and (II) are useful in a marker to indicate the presence or absence of a cancer such as lung cancer.

ABO92145 to ABO92486 and ABP61866 to ABP61992 represent sequences used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanger GR, Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
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                                                       Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine
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protein sequence SEQ ID NO:152
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Retter MW, Durham M, Fange
Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 3080; DB 23;
Pred. No. 8.8e-242;
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  Human lung cancer associated
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07-MAY-2001; 2001US-0850716.
28-JUN-2001; 2001US-0897778.
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McNeill PD, Fanger N,
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                                                                                                                                                                  WO200247534-A2.
                                                                                                              Homo sapiens
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586 AA;
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                                                                                                                          Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                         SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                        SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ
                                                                                           DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                    Polynucleotides encoding lung, tumor polypeptides, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fanger GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henderson
                                                                                                                                                                   GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                                                                                                                                                                                       Human lung tumour L530S protein sequence SEQ ID NO:152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skeiky YAW, Li SX, Kalos MD,
er N, Retter MW, Marnerakis M,
er D, Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lung cancer or stimulating an immune response
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2000US-0662786.
2000US-0685696.
2000US-0735705.
2001US-0850716.
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2000US-0630940.
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                                                                                                                                                                                                                                                       (first entry)
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Carter D,
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N-PSDB; ABL49106.
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02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
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McNeill PD,
Vedvick TS,
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07-MAY-2001;
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stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                               VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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                                                                                                                                 0;
                                                                                                  Length 586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell regulatory protein; p63; mu-deltaNp63 alpha; mouse; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
                                                                                                                                  Indels
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                                                                                              Score 3080; DB 23;
Pred. No. 8.8e-242;
2; Mismatches 2;
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                                                                                                  99.2%;
99.3%;
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                                                                                                               al Similarity 99.3 582; Conservative
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641 AA;
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(IKAW/) IKAWA Y.
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                                                                                                                                                                                                                                                                                                                                                     transactivation domain. The present sequence represents mouse p63 isotype murdeltahp63 alpha. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent cutvities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous cutferentiation, both benign and neoplastic. Deltan isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. Cachexia) and neuronal differentiation and related degenerative cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAN'58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIIVTLETRDGQV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
                                                                                                                                                                                            The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using maplified cDNA possessed a truncated N-terminus, i.e. the ransactivation domain was absent. Additional splice variants were identified by screening a cDNA library with a probe corresponding to exons 5-9 of p63. At least 6 different isotypes exist. Splice variants differing at the C-terminus are designated as alpha, beta can gamma forms, while p63 members differing in the N-terminus are designated as deltan and TA forms, where the deltan form lacks the cransactivation domain. The present sequence represents mouse p63 isotypes and deltan and p63 was detected in a variety of the present sequence represents mouse p63 isotypes and passed passed passed passed p63 was detected in a variety of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 586;
                                                                                                                               New isolated p63 cell regulatory protein for, e.g. treatment
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Pred. No. 1.2e-240;
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                                                                                                                                                                       Claim 23; Fig 18; 161pp; English.
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98.5%;
98US-0087216
            97US-0062076
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Matches 577; Conservative
                                       (HARD ) HARVARD COLLEGE.
                                                                                         WPI; 1999-277595/23
                                                                Yang A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 AA;
                                                                                                       N-PSDB; AAX58581
 29-MAY-1998;
            15-OCT-1997;
                                                                McKeon F,
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                                                                                                                                                                                                       The present sequence represents a human p51 protein, which is related to p53 and has cell proliferation regulation and tumour suppression activity. The p51 gene can be used in the investigation, diagnosis and treatment of diseases such as cancer, with which the p53 family cell proliferation regulation is associated. The p51 protein may be used for screening potential agonists and antagonists of its regulatory function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigation and proliferation
QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
                                                                            DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell proliferation; regulation; cancer;
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/label- DNA_binding_domain
353..397
/label- oligomerisation_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY45247 standard; Protein; 641 AA.
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tumour suppression; diagnosis.
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70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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Best Local Similarity 100.
Matches 572; Conservative
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                Gaps
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                Indels
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        Pred. No. 6.6e-238;
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100.08;
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       Best Local Similarity 100.
Matches 572; Conservative
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15-0CT-1997;
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Indels

97.7%; Score 3033; DB 20; 100.0%; Pred. No. 6.6e-238; ive 0; Mismatches 0;

Length 641;

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which demonstrate certain sequence identity to known tunnour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 5347-29. At least 6 different isotypes exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents human p53 sortype TAp63 alpha. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression differentiation, both benign and neoplastic. DeltaN isotopes of p63 are as dominant negatives towards transactivation by p53 and p63. Cechexia) and neuronal differentiation and related degenerative of sochexia) and neuronal differentiation and related degenerative of standards, and neuronal differentiation and related degenerative of standards, compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of the invention of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour
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                                                                                                                                                                                                       e.g. treatment
                                                                                                                                                                                                New isolated p63 cell regulatory protein for,
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Fig 9; 161pp; English
WPI; 1999-277595/23.
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transgenic animals
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GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 314
                                                                                                                                                                                                                 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
                                                                                                                                                                                                                                                                                                                                                                                                       PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                 ETY EMILKIK ESLELMQYLPQHTIETY RQQQQQQQQQULLLQKQTSIQSPSSYGNSSPPLNK
                                                                                                                                                                                                                                                                              LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
                                                                                                                                                                                                                                                                                                                                          IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; hear shock protein 90 proliferative disease; cellular protein isoform; hear shock protein 91 HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomoncoytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APE; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
                                                                           PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                              MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129
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LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
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                                                                                                                                                                                                                                                                                         protein #2 used to produce a chimeric p53 protein.
                                                                                                                                                                                                                                                                                                                        Human; cytostatic; gene therapy; p53; human tumour.
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Pred. No. 6.6e-238;
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100.0%; Pred. No. o...
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Les 572; Conservative
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N-PSDB; AAF86589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention
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Disclosure; Page 352-354; 389pp; English,

proteins (1), treating cancerous cells containing uncognized traction proliferative diseases associated with mutant protein or cellular protein soforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncognic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform dependent on heat shock protein or cellular protein isoform dependent on heat shock protein or cellular for treating a disease e.g. haematopoietic disorder such as T or B cell imphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML, or a disease characterised by a solid tumour such as appallary thyroid carcinoma, Ewiny's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein. The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous

641 AA; Sequence

70 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129 189 249 309 194 254 314 374 TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 134 554 375 MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 434 LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK 494 74 190 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIJGRQSVLV 15 POYTNIGLINSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP 255 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK 495 IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ Gaps ; Length 641; Indels 97.7%; Score 3033; DB 23; 100.0%; Pred. No. 6.6e-238; ive 0; Mismatches 0; TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586 610 TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE Best Local Similarity 100.0 Matches 572; Conservative 75 250 370 195 315 435 135 555 Query Match ŏ g ò g q ò g g g g δ qq à ŏ à 셤 ŏ ð

Search completed: August 7, 2003, 09:46:26

Job time : 42,4138 secs

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August 7, 2003, 09:42:54; Search time 16.1655 Seconds (without alignments) 1533.769 Million cell updates/sec
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1 MLYLENNAQTQFSEPQYTNL......FNFDMDARRNKQQRIKEEGE 586
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

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SUMMARIES	US-09-643-597-338 US-09-542-615A-338 US-09-643-597-152 US-09-480-884A-152 US-09-542-615A-152	US-09-606-421B-152 US-09-643-597-339 US-09-542-615A-339 US-09-606-421B-339 US-09-643-597-342 US-09-542-615A-342	US-09-606-421B-342 US-09-643-597-343 US-09-642-615A-343 US-09-606-421B-343 US-09-643-597-3344 US-09-542-615A-344 US-09-542-615A-344 US-09-542-615A-344	US-09-643-597-341 US-09-643-597-341 US-09-277-196-2 US-09-606-421B-34 US-09-643-597-340 US-09-643-597-340 US-09-542-615A-34
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Length 586; Indels

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Query Match 99.5%; Best Local Similarity 99.5%; Matches 583; Conservative

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1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIRNGSSSTSPYNTDHAQNSVTAPSPYAQPSP ò g ò g

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Sequence 3, Appli Sequence 20, Appli Sequence 27, Appli Sequence 8, Appli Sequence 8, Appli Sequence 25, Appli Sequence 26, Appli Sequence 2, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli	IE THERAPY
28 1741.5 56.1 635 4 US-09-081-975-3 29 1279.5 41.2 420 4 US-09-277-196-20 31 711.5 22.9 393 1 US-08-047-041A-27 32 711.5 22.9 393 1 US-08-047-041A-27 34 711.5 22.9 393 1 US-08-390-515A-8 34 711.5 22.9 393 1 US-08-390-515A-8 35 707.5 22.8 393 1 US-08-047-041A-25 36 707.5 22.8 393 1 US-08-347-041A-25 37 707.5 22.8 393 1 US-08-347-041A-25 39 707.5 22.8 393 1 US-08-347-041A-26 40 707.5 22.8 393 1 US-08-390-516C-6 40 707.5 22.8 393 1 US-08-390-516C-6 41 707.5 22.8 393 1 US-08-390-515A-	RESULT 1 US-09-643-597-338 Sequence 338, Application US/09643597 Sequence 338, Application US/09643597 Sequence 338, Application US/09643597 SEGUERAL INCORMATION: APPLICANT: Wang, Tongtong APPLICANT: Ralos, Michael D. APPLICANT: Ralos, Michael D. APPLICANT: Ranos, Michael D. APPLICANT: Hosken, Mancy APPLICANT: Hosken, Mancy APPLICANT: Hosken, Nancy APPLICANT: Hosken, Nancy APPLICANT: Henderson, Robert A. APPLICANT: Wang, Aljun APPLICANT: Wendell, Particle D. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 21012.455011 CURRENT APPLICATION NUMBER: US/09/643,597 CURRENT FILING DATE: 2000-08-21 NUMBER OF SEQ ID NOS: 369 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 338 LENGTH: 586 TTYPE: PRT CREATH: SHE

us-09-538-106-16.rai

DD 301 SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQQQHQHLQISGQ 360	QY 361 SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTTPDGMGANIPMMGTHMPMAG 420	Qy 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480	QY 481 QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR 540	Qy 541 GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586	[2]B-338	Sequence 389, Application US/USOUGALIB Sequence 380, Application US/USOUGALIB GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Bangur, Chaitanya S. APPLICANT: Brangur, Chaitanya S. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND STORMER TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER CURRENT FAPLICATION UNBER: USO/09/606,421B CURRENT FILING DATE: 2000-06-28 NUMBER OF SEQ ID NOS: 358 LENGTH: 586 TYPE: PRT CREANISM: HOMO Sapiens US-09-606-411B-338	Query Match 99.5%; Score 3087; DB 4; Length 586; Best Local Similarity 99.5%; Pred. No. 2.8e-278; Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	OY 1 MLYLENNAQTQESEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60	QY 61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQ1AKTCPIQIK 120	Qy 121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180	Qy 181 YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNEMCNSSCVGGMNRRPILIIVTLETRDGQV 240	QY 241 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR 300	Qy 301 SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ 360
	QY 301 SPDDBLLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQHQHLLQKQTSIQ 360 	QY 361 SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPPTTPDGMGANIPMNGTHMPMAG 420	QY 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480	QY 481 QIBHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR 540	Qy 541 GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586 	RESULT 2 US-09-542-615A-338 Sequence 338, Application US/09542615A Sequence 338, Application US/09542615A Sequence 338, Application US/09542615A Sequence 338, Application US/09542615A SEQUENCE NOTION SEQUENCE TO SEQUENCE SEQUENC	Ouery Match Query Match 99.5%; Score 3087; DB 4; Length 586; Best Local Smilarity 99.5%; Pred, No. 2.8e-278; Matches 583: Onecrusting	1 MLYLENNAQTOESEPOYTHIGLLNSWDQQIRQSSSTSPYN 1 HITHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	PIQIK 	NSHAQ - -	YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNEWCNSSCVGGMRRPILLIVTLETRDGQV 	241 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR [301

	RESULT 5 US-09-480-884A-152 S-09-480-884A-152	Query Match 99.2%; Score 3080; DB 4; Length 586; Best Local Similarity 99.3%; Pred. No. 1.3e-277; Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0; QY 1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120	OY 181 YVEDPITGROSVLVPYEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGOV 240
Db 301 SPDDELLYLPVRGRETYEMLLKIKESLELMOYLPQHTIETYRQQQQQQQQHQHLLQKGTSIQ 360 361 SPSSYGNSSPPLAKMNSMNKLPSVSQLINPQQRAALTPTTIPDGMGANIPMAGTHMPMAG 420 11111111111111111111111111111111111	RESULT 4 US-09-643-597-152 US-09-643-597-152 Sequence 152, Application US/09643597 Fatent No. 6426072 GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Ralos, Michael D. APPLICANT: Bangui, Chaltanya S. APPLICANT: Rang, Aljun APPLICANT: Mangy APPLICANT: Mangy APPLICANT: Mangy APPLICANT: Mangy APPLICANT: Mangy APPLICANT: Mangy APPLICANT: Moneil, Patricia D. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C11 CURRENT APPLICATION NUMBER: US/09/643.597 CURRENT FILING DATE: 2000-08-21 NUMBER OF SEQ ID NOS: 369 SEO TO NO 15-25CE OF WINDOWS VERSION 3.0	ENGTH: 586 YPE: PRT RGANISM: Homo sapien -643:597-152 FY Match 99.2%; Score 3080; DB 4; Length 586; L Local Similarity 99.3%; Pred. No. 1.3e-277;	VALIVE 2; MISMATCI TOPSEPQYTNLGLLNSMDQQIC I TOPSEPQYTNLGLLNSMDQQIC ALPSNTDYPGPHSFDVSFQQSS	121 VMTPPPQGAVIRAMPVKKAEHVTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGOIAPSSHLIRVEGNSHAQ 181 VVEDPITGRQSVLVPYEPPQVGTEFTTVLVRPMCNSSCVGGMNRRPILIIVTLETRDGQV 181 VVEDPITGRQSVLVPYEPPQVGTEFTTVLVRPMCNSSCVGGMNRRPILIIVTLETRDGQV 181 VVEDPITGRQSVLVPYEPPQVGTEFTTVLVRPMCNSSCVGGMNRRPILIIVTLETRDGQV 241 LGRRCFEARICACPGRDRRADEDSIRKQQVSDSTKNODGTKRPFRQNTHGIQMTSIKKRR 1111111111111111111111111111111111

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: Lambar Course 
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Pred. No. 1.3e-277;
2; Mismatches 2;
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APPLICANT: Fan, Liquu
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya
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Best Local Similarity 99.3%;
Matches 582; Conservative
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                                                                                                                                                                                                                                                                   US-09-606-421B-152
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Pred. No. 1.3e-277;
2; Mismatches 2;
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Patent No. 6518256
GENERAL INFORMATION:
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy A.
Fanger, Gary R.
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Best Local Similarity 99.3
Matches 582; Conservative
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ORGANISM: Homo
-09-643-597-339
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APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
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                                       MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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Skeiky, Yas
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US-09-542-615A-339
'Sequence 339, App
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APPLICANT: Franger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FO
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.45508
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
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Fan, Liqun
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Pred. No. 8e-273;
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tiqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45509
CURRENT APPLICATION MUMBER: US/09/606,421B
CURRENT FILLING DATE: 2000-06-28
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US-09-606-421B-339
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
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GENERAL TOTAL
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TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
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US-09-643-597-342
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IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
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Fanger, Gary R.
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Fan, Liqun
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CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FRSLSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo saplens
US-09-542-615A-342
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
FILE REFERENCE: 210121.455C8
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Kalos, Michael D.
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APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Nancy
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Wang, Aijun
APPLICANT: AING
APPLICANT: Wang, Michael D.
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GENERAL INFORMATION:
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                        TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
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    TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                   IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
                                                                                                      IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRETLRQ
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Pred. No. 2.1e-27
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494

528 434 468 374 408 314 348 254 288 194

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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: McNeill, Patricia D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHOD:
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG C/
TITLE OF INVENTION: NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEO ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-643-597-343
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Best Local :
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                           421
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o. 6426072
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DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
                                                                                                  VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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Pred. No. 1.6e-216;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 461;
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METITLE OF INVENTION: AND DIAGNOSIS OF FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTMARE: FastSEQ for Windows Versic SEQ ID NO 343
FENCTH: 461
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-343
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Best Local Similarity
                              421
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                                                                                                                                                                                                                                                      FastSEQ for Windows Version
                DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
                                                                              SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                            SPDDELLYLPYRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
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DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                             SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Pred. No. 1.6e-21
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Search co completed: August ne : 18.1655 secs 7, 2003, 09:54:54

> 420 420 360 360 300 300 240 240 180

RESULT 15 US-09-542-615A-343 ; Sequence 343, Application ; Patent No. 6518256 ; GENERAL INFORMATION:

US/09542615A

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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3104
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1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO. 1 2 3 5 6 6 7 8 8	Score 3087 3087 3087 3080 3080 3080 3080 3080	Match 99.5 99.5 99.2 99.2 99.2 99.2	Length 586 586 586 586 641	DB	US-09-735-705-338 US-09-850-716A-338 US-09-850-778-338 US-09-850-778-715-2 US-09-850-716A-152 US-09-897-778-152 US-09-850-716A-339 US-09-850-716A-339
–	3087	99.5	586	9	US-09-735-705-
2	3087	99.5	586	10	US-09-850-716
ω	3087	99.5	586	10	US-09-897-778-
	3080	99.2	586	ø	US-09-735-705-1
₅	3080	99.2	586		US-09-850-716#
6	3080	99.2	586		us-09-897-778-
7	3080	99.2	586	11	US-09-466-396A
8	3029	97.6	641	9	US-09-735-705-33
9	3029	97.6	641	10	US-09-850-716A-
10	3029	97.6	641	10	us-09-897-778-3
11	3025	97.5	680	9	US-09-735-705-3
12	3025	97.5	680	10	US-09-850-716A
13	3025	97.5	680	10	US-09-897-778-342
14	2421	78.0	461	9	US-09-735-705-343
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28,	Sequence 36, Appl		ω	78,	<u>ب</u>	-	2		4,	é	4	9	e 3,	32,		10	ω		e 34	340	Sequence 2, Appli	Sequence 341, App	e 341,	341,	_	344,	e 344,	Sequence 344, App	date to the posture

ALIGNMENTS

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; SOFTWARE: FastSEQ for Wi
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-338
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US-09-735-705-338; A
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Best Local Similarity
Matches 583; Conserv
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                                                                                                                                                                                                                   APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455014
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER O SED ID NOS: 419
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                1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
MLYLENNAQTQFSEPQYTNLGLLNSMDQQIRNGSSSTSPYNTDHAQNSVTAPSPYAQPSP 60
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In, Liqun
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Bangur, Chaitanya S.
                                                                Conservative
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                                                                             99.5%;
                                                             Score 3087; DB 9;
Pred. No. 7.9e-248;
1; Mismatches 2;
                                                                                           Length 586;
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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOPTWARE: FESTSEEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-338
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US-09-850-716A-338
; Sequence 338, Application US/09850716A
; Patent No. US20020115139A1
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Similarity 99.5%;
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Pred. No. 7.9e-248;
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CARTER, LORANTS.

CARTER, DARRICK

LIFLICANT: Wattanabe, Yoshihiro

APPLICANT: Henderson, Robert A.

APPLICANT: Peckham, David W.

APPLICANT: Fenger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C16

CURRENT APPLICATION NUMBER: US/09/897,778

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SEQ ID NO 338

LENGTH : S86

TYPE: PRT

ORGANIC:
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Sequence 338, Application US/09897778; Patent No. US20020147143A1; GENERAL INFORMATION:
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                                                                                                                                                                       ; Score 3087; D; Pred. No. 7.9e 1; Mismatches
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APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILLING DATE: 2000-12-12
UMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
SEQ ID NO 152
SEQ ID NO 152
TYPE: PRT
ORGANISM: Homo sapien
US-09-735-705-152
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APPLICANT: Wang, To
APPLICANT: Fan, Liq
APPLICANT: Kalos, M
APPLICANT: Bangur,
APPLICANT: Hosken,
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 McNeill, Patricia D.
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                                                                                                                                      Conservative
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Pred. No. 3e-2,
2; Mismatches
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                        VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                    TEDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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                                                                       VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPSSHLIRVEGNSHAQ
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99.3%;
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Pred. No. 3e-247;
2; Mismatches
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GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
                                                                                                   QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETR
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GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
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GENERAL INFORMATION:
APPLICANT: KALOS, Michael D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Retter, Marc W.
ITILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: HOMO Sapien
US-09-850-716A-152

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Length Indels

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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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Best Local
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APPLICANT: Fanges
APPLICANT: Vedvic
APPLICANT: Cartes
APPLICANT: Watang
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APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
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                                                                                                                                                                                                                                                                       Local
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Similarity 99.3%;
                                                     YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                               TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
            LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                        YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                           VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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Watanabe, Yoshihiro
Henderson, Robert A.
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Vedvick, Thomas S.
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467
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Pred. No. 3e-247;
2; Mismatches
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PUBLICATION NO. US20030119763A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FO
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45504
CURRENT FILING DATE: 199-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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                            SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Pred. No. 3e-247;
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LUNG CANCER
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Qy 15 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74 111111111111111111111111111111111111	SOFTMARE: FastSEQ for Windows Version 3.0 SEQ ID NO 339 LENGTH: 641 TYPE: PRT ORGANISM: Homo sapiens US-09-735-705-339 Query Match Best Local Similarity 99.8%; Pred. No. 5.9e-243; Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Sequence 339, Application US/09735705 Patent No. US20020052339A1 GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Kalos, Michael D. APPLICANT: Kalos, Michael D. APPLICANT: Bangur, Chaitanya S. APPLICANT: Bangur, Chaitanya S. APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Li, Samuel X. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Fanger, Neil APPLICANT: Fanger, Neil TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C14 CURRENT APPLICATION NUMBER: US/09/735,705 LUNDBER OF SEO ID NOS: 419	Qy 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Qy 135 PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194	Query Ma Best Loc Matches	RESULT 9 US-09-850-716A-339 US-09-850-716A-339 ; Sequence 339, Application US/09850716A ; Patent NO. US20020113139A1 ; GENERAL INFORMATION: APPLICANT: Kalos, Michael D. APPLICANT: KALOS, Michael D. APPLICANT: Retter, Marc W. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C15 ; CURRENT APPLICATION NUMBER: US/09/850,716A ; CURRENT FILING DATE: 2001-05-07 ; NUMBER OF SEQ ID NOS: 440 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 339 ; LENGTH: 641 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-850-716A-339	Db 430 MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 489 Qy 435 LSMPSTSHCTPPPPPYPTDCSIVSFLARLGCSSCLDYFTTOGLTTIYQIEHYSMDDLASLK 494

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LENGTH: 641
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APPLICANT: Marne.
APPLICANT: Fange.
APPLICANT: Vedvi.
APPLICANT: Carte.
APPLICANT: Watan
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APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ 1D NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
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  495
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                        MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
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Henderson, Robert A.
Peckham, David W.
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Pred. No. 5.9e-243;
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APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Patricia D.
APPLICANT: Monelil, Patricia D.
APPLICANT: MONelil, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND TITLE OF INVENTION: AND DIAGNOSIS OF FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTMARE: FastSEQ for Windows Versic SEQ ID NO 342
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US-09-735-705-342
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: Patent No. US20020052329A1
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Fanger, Gary R.
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99.8%;
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GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: KCNEill, Patricia D.
APPLICANT: Retter, Warc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                       IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
                                                                                              LSMPSTSQCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK
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Pred. No. 1.4e-242;
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CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
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APPLICANT: Warner
APPLICANT: Fanger
APPLICANT: Vedvic
APPLICANT: Carter
APPLICANT: Watana
APPLICANT: Hender
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            TISEPPRDEWNDENFDMDARRNKQQRIKEEGE 586
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

APPLICANT: Fanger, Neil

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SEQ ID NO 343

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Best Local Similarity
Matches 456; Conserv
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                                                                                               SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                               SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Fan, Liqun
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Bangur, Chaitanya
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CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIACNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                     SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                       SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Pred. No. 1.1e-192;
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Search completed: August Job time: 26.0181 secs 7,

RESULT 15 US-09-850-716A-343

Sequence 343, Application Patent No. US20020115139A1

Application US/09850716A

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                    MLYLENNAQTQFSEPQYTNL.....FNFDMDARRNKQQRIKEEGE 586
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RESULT A29376

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299

167 PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP 226

RGHLVRVEGNQRSEYMEDGNTLRHSVLVPYEPPQVGSECTTVLYNFMCNSSCMGGMNRRP

339 300

ETYRQQ 344

360 DKYRQK 365

Query Match 27.0%; Score 839.5; DB Best Local Similarity 55.2%; Pred. No. 8e-51; Matches 169; Conservative 47; Mismatches 7	ne product of r antigen p53 division contrice: zinc (Cys, y1-RNA (Ser) (NA DEF> GB:M75145; NID:g213828 ce: liver	A;Title: Rainbow trout p53: cDNA cloning and biochemical A;Reference number: JH0631; MUID:92210006; PMID:1339362 A;Accession: JH0631	C;ACCESSION: JHU631 R;de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; Gene 112 2/1-2/5 1002	RESULT 1 JH0631 cellular tumor antigen p53 - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	ALIGNMENTS	122.5 3.9 1366 2	. 123 4.0 3942 . 122 5 3 9 1221	123 4.0 2232 2	40 123 4.0 969 2 T15446	123.5 4.0 921 2	123.5 4.0 862 2 123.5 4.0 921 2	124 4.0 826 2	124 4.0 590	124.5 4.0 864 2	124.5 4.0 864 2	124.5 4.0 811 2	124.5 4.0 533	
1; Length 396; 79; Indels 11; Gaps 6;	a tumor suppressor gene, p53, whose inactiv ol; DNA binding; homotetramer; nucleus; pho His, Cys, Cys) #status predicted covalent) #status predicted	AA49605.1; PID:g213829	emical characterization. 39362	y, C.; May, P.; Soussi, T.	<pre>#text_change 10-Sep-1999</pre>		F7H2.12 protein -	Bassoon protein -	hypothetical prote	hypothetical prote	TBP-associated fac	nomeotic protein C	hypoxia-inducible	cell pattern forma	hypothetical prote	hypothetical prote	hypoxia-inducible	developmental cont	

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A;Title: Nucleotide sequence of a cDNA encoding the chicken A;Reference number: S02193; MUID:89083584; PMID:3060861 A;Accession: S02193
A;Molecule type: mRNA A;Residues: 1-367 <S0U>
                                                                                                                                                                                                    cellular tumor antigen p53 - chicken
N;Alternate names: nuclear oncoprotein p53
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S02193
R;Soussi T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
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A;Residues: 1-293,295-363 <HOE>
A;Residues: 1-293,295-363 <HOE>
A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
submitted to the EMBL Data Library, March 1994
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A;Title: Overexpression of wild-type p53 interferes with normal development A;Reference number: 151639; MUID:94134403; PMID:8302570
A;Accession: S61531
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C;Accession: A29376; S61531; S72313; I51639
C;Accession: A29376; A29376; S61531; S72313; I51639
C;Accession: A29376; A29376; S61531; S72313; I51639
C;Accession: A29376; S61531; A29376; A29
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S02193
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C;Superfamily: cellular tumor antigen p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nu:
F;150,153,217/Binding site: zinc (Cys, His, Cys, Cys) *Status predicted
F;362/Binding site: phosphoryl-RNA (Ser) (covalent) *Status predicted
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A; Accession: A29376
A; Molecule type: mRNA
A; Molecule: 1-563 < SOU>
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A;Title: Cloning and characterization of a cDNA from Xenopus
A:Deference number: A29376; MUID:88143684; PMID:2830576
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A; Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOW>
A; Cross-references: EMBL: X77546; NID: 9468513; P
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A; Accession: S72313
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R;Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
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42; Mismatches
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RESULT 4
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A;Molecule type: mRNA
A;Residues: 1-386 <DEQ>
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: S51648
C;Accession: S51648
R;Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R
submitted to the EMBL Data Library, September 1994
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                                                                                                                                                                                                                                                                                                                                 ENNAQTQFSEPQYTNLGLL----NSMDQQIQNGSSSTSPYN----TDHAQNSVTAP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence
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                                                                                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                                                                                                        Score 744; DB 1;
Pred. No. 3.4e-44;
5; Mismatches 120
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A; Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2 C; Superfamily: cellular tumor antigen p53 C; Superfamily: cellular tumor antigen p53 C; Septens: apoptosis; cell division control; DNA binding; homotetramer; nuc F;174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
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A;Title: Structure of the rat p53 tumor suppressor gene. A;Reference number: S41149; MUID:93181268; PMID:8441680
A;Accession: S41149
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A;Title: Nucleotide sequence of a cDNA encoding the rat A;Reference number: S02192; MUID:89083585; PMID:3060862
A;Accession: S02192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S02192; S41149
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A;Note: the nucleotide sequence was submitted to the EMBL C;Genetics:
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A; Residues: 1-173, 'W', 175-391 <HUL>
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A; Residues: 1-391 <SOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: gene p53 protein; nuclear oncoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellular tumor antigen p53 - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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367
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                                                                                                                                                                                                          GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFE
                                                                                                                                                                                                                                                                                                                                                                                                                                          TNLGLLNSMDQ------QIQNGSSSTSPYNTDHAQNSYT-APSPYAQPSSTFDALSPS
NSSPPLNK - - - MNSMNKLPSVSQL
                                     FTLKIRGRERFEMFRELNEALELK----
                                                                     LYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYG
                                                                                                             VRVCACPGRDRRTEEENFRKKEEHCPELPPGSAKRALPTST----SSSPQQKKKPLDGEY
                                                                                                                                              ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL
                                                                                                                                                                                      FRHSVVVPYEPPEVGSDYTTIHYKYMCNSSCMGGMNRRPILTITLEDSSGNLLGRDSFE
                                                                                                                                                                                                                                                                  TRVRAMAIYKKSQHMTEVVRRCPHHE----RCSDGDGLAPPQHLIRVEGNPYAEYLDDRQT
                                                                                                                                                                                                                                                                                                     AVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQ-IAPPSHLIRVEGNSHAQYVEDPIT
                                                                                                                                                                                                                                                                                                                                           -- VPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSISLNKLFCQLAKTCPVQLWVTSTPPPG
                                                                                                                                                                                                                                                                                                                                                                                 PAIPSNIDYPGPHSFDVSFQQSSTAKSATWIYSTELKKLYCQIAKTCPIQIKVMTPPPQG
                                                                                                                                                                                                                                                                                                                                                                                                                      TATGSPNSMEDLFLPQDVAELLEGPEEALQVSAPAAQEPGTEAPAPVAPASATPWPLSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RALPTNT----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALEL-----KDALDG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPFRQNTHGIQMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIET 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 723; DB 1;
Pred. No. 9.8e-43;
4; Mismatches 116
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N;Alternate names: tumor suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #te
C;Accession: JH0633
R;Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A;Title: The cDNA cloning and immunological characteri:
A;Reference number: JH0633; MUID:92210007; PMID:1555777
A;Accession: JH0633
A:Mclacenis
                                                                                                                                                                                                 cellular tumor antigen p53 [validated] - human
N;Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformati
C;Species: Homo sapiens (man)
C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C;Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397;
4905; I58354; I78850; I52681; S60153
R;Lamb, P.; Crawford, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuc F;179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
A;Cross-references: EMBL:X01405; R;Buchman, V.L.; Chumakov, P.M.;
                                                   A; Molecule type: DNA
A; Residues: 1-393 <LAM>
                                                                                                A; Title: Characterization of the human p53 A; Reference number: A25224; MUID:87064416; A; Accession: A25224
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A; Cross-references: GB:M75144; NID:g191414;
A; Experimental source: kidney, strain MP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDDELLYLPVRGRETYEMLLKIKESLEL 329
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GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987 Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 712; DB 1; Length 396; Pred. No. 5.8e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353
                                                                                                                              gene.
PMID:2946935
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                                                                                                                                                                                                                                                                                                                                     oncoprotein p53; transformation suppr
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A; Molecule type: mRNA
A; Rosidues: 1-71, 'p', 3-272, 'H', 274-393 <HAR>
A; Residues: 1-71, 'p', 3-272, 'H', 274-393 <HAR>
A; Residues: 1-71, 'p', 3-272, 'H', 274-393 <HAR>
A; Experimental source: clone pR4-2, cell line A431
R; Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, Mol. Cell. Blol. 6, 4650-4656, 1986
A; Title: Molecular basis for heterogeneity of the human p53 protein.
A; Reference number: A93086; MUID:87089826; PMID:3025664
A; Accession: A25397
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-71, 'p',73-78,'T',80-393 <HAR2>
A; Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R; Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford,
Mol. Cell. Biol. 7, 961-963, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Molecule type: mRNA
A;Residues: 1-71,'p',73-93 <ZAK>
A;Residues: 1-71,'p',73-93 <ZAK>
A;Residues: 1-71,'p',73-93 <ZAK>
A;Residues: 1-71,'p',73-93 <ZAK>
A;Residues: 1-71,'p',73-93 <ZAK-
A;Residues: 1-71,'p',73-93 <ZAK-
A;References: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
R;Harlow, E; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
Mol. Cell. Biol. 5, 1601-1610, 1985
Mol. Cell. Biol. 5, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
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A;Title: Human p53 cellular tumor antigen: cDNA sequence and e: A;Reference number: A22837; MUID:85230577; PMID:4006916
A;Accession: A22837
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A; Residues: 1-71, 'p', 7-393 <BUC2>
A; Residues: 1-71, 'p', 7-393 <BUC2>
A; Cross-references: EMBL: M22898; NID: g189474; PIDN: AAA59988.1; PID: g189476
A; Note: this 72-Pro allele was found in both normal and malignant cell line
R; Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
submitted to the EMBL Data Library, August 1990
                                                                                                                                                                            A; Molecule type: mRNA; DNA
A; Residues: 66-71, 'p',73-79 <mKI2>
A; Experimental source: clone lambda C113
A; Note: 72-Cys was also found, and appear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-78,'T',80-393 <HARI>
A;Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A;Experimental_source: clone p53-H-1, transformed hybridoma SV-80 cell line
   A; Experimental source: clone R; Farrell, P.J.; Allan, G.J.;
                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 7, 961-963, 1987
A;Title: Primary structure polymorphism at amino acid residue 72 of human p53
A;Reference number: $42452; MUID:87144273; PMID:3547088
A;Accession: $42452
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                                                                        A; Molecule type: mRNA; DNA
A; Residues: 66-79 < MKI3>
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A; Residues: 1-71, 'P', 7
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A; Residues: 101-393 <MKI1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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A; Accession: S40773
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A; Residues: 1-393 <BUC1>
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                                                                                                                                                 S42453
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J6K
; Shanahan,
                                                                                                                                                                                appears
F.; Vousden,
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K.H.;
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                                                                                                                                                                            polymorphism
   Crook,
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L.; Benchimol,
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A; Nolecule type: mRNA
A; Nolecule type: mRNA
A; Residues: 1-253, 'D', 255-393 <F11>
A; Residues: 1-253, 'D', 255-393 <F11>
A; Cross-references: EMBL: X60920; NID::g506452; PIDN: CAA42635.1; PID::g506453
A; Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 19:
A; Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 19:
A; Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 19:
A; Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 19:
                                                                                                                                                                                                                                                                            Nucleic Acids Res. 19, 6977, 1991
A;Title: An Alu polymorphism intragenic to the TP53 gene A;Reference number: I38093; MUID:92107726; PMID:1762941 A;Accession: I38093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-247,'Q',249-393 <F08>
A; Cross-references: EMBL:X60017; NID:g506446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A; Cross-references: EMBL: X60016; NID: g506444;
                      A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214 R;Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, Cancer Res. 51, 5800-5805, 1991 A;Tille: p53 gene mutations in gastric cancer metastases and in gastric can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A; Cross-references: EMBL: X60018; NID: 9506448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-247, 'Q', 249-393 <F06>
A; Cross-references: EMBL: X60015; NID: g506442;
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A; Residues: 1-245, 'T', 247-393
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A; Residues: 1-192, 'R',194-393 <F02>
A; Cross-references: EMBL:X60011; NID:g506434;
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A;Title: p53 is frequently mutated in Burkitt's lymphoma cell lines A;Reference number: 138082; MUID:92007731; PMID:1915267
A;Accession: I38082
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-393 <FUT>
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A; Residues: 1-212,'Q',214-393 <F10>
A; Cross-references: EMBL:X60019; NID:g506450;
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A; Residues: 1-236, 'I', 238-393 <F05>
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A; Cross-references: EMBL: X60013; NID: g506438;
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A; Residues: 1-393 <F03>
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gene mutations in gastric cancer metastases number: A44905; MUID:92034678; PMID:1933850
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A; Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIP:63158)
A; Note: mutation from a liver metastasis of a gastric cancer R; Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L. Oncogene 6, 1067-1071, 1991
A; Title: Tan of the
RESULT 8
S06594
cellular
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A; Residues: 3-44 <PET>
R; Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 327-331, /ODISFOKENC' <CHO>
A;Residues: 327-331, /ODISFOKENC' <CHO>
A;Residues: 327-331, /ODISFOKENC' <CHO>
A;CHOS-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A;Note: mutant sequence with altered splicing and termination expressed in Mc
R;Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A;Title: Mapping of linear epitopes recognized by monoclonal antibodies with
A;Reference number: S60151; MUID:96133682; PMID:8552047
A;Accession: S60153
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A;Residues: 274-277, /S',279-282 <HEN2>
A;Residues: 274-277, /S',279-282 <HEN2>
A;Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1;
R;Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A;Title: Alternative splicing of the p53 tumor suppressor general companies. IS2681; MUID:94036762; PMID:8221626
A;Accession: IS2681
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A;Cross-references: GB:S41969; NID:g1679931; PIDN:AAB19324.1;
A;Accession: I78850
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  antigen
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DNNS53
C:Blular tumor antigen p53 - mouse
N;Alternate names: oncoprotein p53
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
                                                                                                                                                                                                                                                                                             R;Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
B;Title: Primary structure of DNA complementary to murine A;Reference number: S06336; MUID:88221682; PMID:3329909
A;Accession: S06336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular A;Reference number: A22739; MUID:85027173; PMID:6092064
A;Accession: A22739
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Nuclect Acids Res. 17, 8375, 1989
A;Title: Nuclectide sequence of a cDNA encoding the monkey
A;Reference number: S06594; MUID:90045967; PMID:2530498
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S06594
A;MoLecule type: mRNA A;MoLecule type: mRNA A;Residues: 1-159,'H',161-167,'G',169-233,'I',235-390 A;Residues: GB:X01237; GB:K01700; NID:953575 R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E
                                                                                                  A; Reference number: A; Accession: A02684
                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-134, 'V', 136-390 <CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-134, 'V', 136-390 <BIE>
A; Cross-references: GB: X00876; NID:
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                                                                                                                                                    A; Title:
                                                                                                                                                                         Nature 306, 594-597, 1983
                                                                                                                                                                                               R; Zakut-Houri, R.; Oren, M.;
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                                                                                                                         A single gene and a pseudogene for number: A02684; MUID:84068204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POHLIRVEGNLEVEYSDDRNTFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MFCQLAKTCPVQLWVDSTPPPGSRVRAMAIYKQSQHMTEVVRRCPHHE---RCSDSDGLAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APSPYAQPSSTFDALSP----SPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTHGIQMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQ
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                                                                                                                                                                                               Bienz,
                                                                                                                                                                                                                                                                                                                                                                                                                        NID:g871420; PIDN:CAA25420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 703; DB 1;
Pred. No. 2.4e-41;
                                                                                                                                                                                               B.; Lavie,
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PMID:6646235
                                                                                                                                                                                                  V.; Hazum,
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E.; Shohat,

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Rotter,

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F;267-283/Region: conserved region V
F;313-319/Region: nuclear location signal
F;319-357/Region: tetramer association
F;7,9,12-18,23-37/Binding site: phosphate (Ser) (covalent) #status predicted
F;7,9,12-18,23-37/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;173,176,235,239/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F;312/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
F;389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-47, 'R', '49-78, 'QW', 82-390 <RES>
A;Cross references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
C;Comment: This DNA-binding protein plays an essential role in the regula
C;Comment: The tetramer association region may exhibit a beta-turn, beta-
C;Comment: The tetramer association region may exhibit a beta-turn, beta-
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer;
F;1-44/Domain: transcription activation #status predicted <TRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:99-289/Domain: DNA-binding core #status
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-167, 'G', 169-390 < ARA3>
A; Residues: 1-167, 'G', 169-390 < ARA3>
A; Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1;
A; Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
A; Title: Cloning and expression analysis of full length mouse c
A; Reference number: 148703; MUID:84272240; PMID:6379601
A; Accession: 148703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:M13873
R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; submitted to the EMBL Data Library, July 1988
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A; Residues: 1-167, 'G', 169-233, 'I', 235-390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S40014
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Best Local Similarity
Matches 147; Conserv
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QHTIE-
                                                                                           KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
                                                                                                                                                                                           NSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDST
                                                                                                                                                                                                                                           --RCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYEPPEAGSEYTTIHYKYMC
                                                                                                                                                                                                                                                               SREFNEGQ-IAPPSHLIRVEGNSHAQYVEDPTTGRQSVLVPYEPPQVGTEFTTVLYNFMC
                                                                                                                                                                                                                                                                                                                                        VMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE-
                                                                                                                                                                                                                                                                                                                                                                       ATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHEL
                                                LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---
                                                                                                                                             NSSCMGGMNRRPILTITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                         AQDPVTETPGPVA-----PAPATPWPLSSFVPSQKTYQGNYGFHLGFLQSGTAKS
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43.2%; Pred. No. 2.8e-41;
tive 54; Mismatches 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 390;
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C;Superfamily: cel
C;Keywords: liver;
                                                                                                                                                                                                                           R;Lee, H.; Larner, J.M.; Hamlin, J.L. Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster A;Reference number: JC6176; MUID:97183659; PMID:9031625
A;Contents: liver
                                                                                                                                                                                                                                                                                                                                         tumor suppressor protein p53 - Chinese hamster C;Speckes: Cricetulus griseus (Chinese hamster) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 C;Accession: JC6176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: p53
C;Superfamily: cellular tumor antigen
C;Keywords: tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Le Goas, F.; May, P.; Ronco, P.; de Fromentel, C.C. Gene 185, 169-173, 1997
A;Title: cDNA cloning and immunological characterization A;Reference number: JC6193; MUID:97208869; PMID:9055811
A;Accession: JC6193
                                            A;Gene: p53
                                                                                                             C; Comment:
                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-393 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-391 <LEA>
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C;Accession: JC6193
                                                                      C; Genetics:
                                                                                             iption,
                                                                                                             A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230 C;Comment: This protein is a multimer, it plays the central role in a complex DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       JC6176
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                                                                                                                                                                                                         A; Accession: JC6176
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Pred. No. 3.9e-41;
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A; Recession: 534/0
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-381 <HAN>
A; Rosidues: 1-381 <HAN>
A; Residues: 1-381 <HAN>
A; Rosidues: 1-381 <HAN
A; Rosidues: 1-381 <H
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Nucleic Acids Res. 20, 1979-1981, 1992
A;Title: Alternatively spliced p53 RNA in transformed and A;Reference number: S35478; MUID:92253421; PMID:1579500
A;Accession: S35478
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A; Accession: S38824
A; Molecule type: mRNA
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;313-319/Region: nuclear location signal
;319-357/Region: tetramer association
;319-357/Region: tetramer association
;719-12.18.23.37/Binding site: phosphate (Ser) (covalent) #status predicted
;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
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Pred. No. 5.9e-41;
2; Mismatches 93;
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A; Title: The canine p53 gene is subject to somatic mut A; Reference number: I46226; MUID:95150524; PMID:784784 A; Reference number: I46226; MUID:95150524; PMID:784784 A; Residues: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-77 < DEV> A; Cross-references: GB:L27630; NID:g508454; PIDN:AAC37 C; Genetics: A; Gene: p53 A; Introns: 24/1; 61/3 C; Superfamily: cellular tumor antigen p53
A; Reference n
A; Accession:
                                                               hypothetical protein C17G1.4 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc. Accession: T19361 R; White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ceilular tumor antigen p53 - dog (fragment)
(;Species: Canis lupus familiaris (dog)
(;Species: Canis lupus familiaris (dog)
(;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
(;Accession: I46226
R;Devilee, P; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, Anticancer Res. 14, 2039-2046, 1994
A;Title: The canine p53 gene is subject to somatic mutations in thypoid carcinoma.
A;Reference number: I46226; MUID:95150524; PMID:7847847
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                             139 KAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP
                                                                                                                                                                                                                                                                                     199 PQVGTEFTTVLYNFMCNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 AHATEESGDSRAHSSLQPRAFQALIKEES
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    o the EMBL Data number: Z19114 : T19361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --RCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYEPPEAGSEYTTIHYKYMC
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                                                                                                                                                                                                                                                                                                                                                    KSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRYTFRHSVVVPYEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                               Library,
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Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 259.5; DB 2
Pred. No. 1.7e-11;
                                             August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 15
JC6093
                 A:Cross-references: GB:U62542;
A:Experimental source: embryo
C:Genetics:
                                                                                                                    R;Gregory, S.L.; Kortschak, R.D.; Kallonis, B.; Saint, R. Mol. Cell. Biol. 16, 792-799, 1996
A;Title: Characterization of the dead ringer gene identifies A;Reference number: JC6093; MUID:96182081; PMID:8622680
A;Accession: JC6093
                                                                                                                                                                                                                                          dead ringer nuclear protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
A;Gene:
                                                                             A; Residues: 1-901 <GRE>
                                                                                                                                                                                                                             C; Accession: JC6093
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A; Introns: 40/3; 98/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; 1
A;Molecule type: DNA
A;Residues: 1-925 <WIL>
                                                                                                   A; Molecule type: mRNA
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Best Local
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nes 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             582 DTLHVGPNDKVHPQVEKHYFSRKRQQLRVPYP-----EGINSHTTPPTEPNTFGFMQGN
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                                                       NID:g1480739; PIDN:AAB05771.1; PID:g1480740
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Pred. No. 0.014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 PKRKEFLDDLFSFMQKRGTPINRLPIMAKSVLDLYELYNLVIARGGLVDVINKKLWQEII 341
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Nature 399:814-817(1999).
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Kharbanda S., Weichselbaum
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                   TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
INDUCTION: NOT INDUCED BY DNA DAMAGE.
DWAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRA DINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT TO THE ABL TYROSINE KINASE SH3 DOMAIN.
DISEASE: MAPS TO A CHOMOSOME REGION FREQUENTLY MUTATED IN CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSER
                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN.

SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TYROSINE KINASE SH3 DOMAIN: ISOFORM BETA INTERACTS HOAND WITH P53, WHEREAS ISOFORM ALDHA DOES NOT. ISOFORM INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. IS INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALL INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl.
 NEUROBLASTOMA AND OLIGODENDROGLIOMA SIMILARITY: BELONGS TO THE P53 FAMII
                                                                                                                                                                                                                          Name=Epsilon;
IsoId=015350-5;
                                                                                                                                                                                                                                                                                                                                                                                       SÜBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                           Event-Alternative splicing; Named isoforms-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              emerging p53 gene
atl. Cancer Inst. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is regulated by tyrosine kinase c-Abl in the apoptotic response
                                                                                                                                                                                    Note=The splicing original reading frame to t
                                                                                                                                                                                                                                                                      IsoId=015350-3; Sequence=VSP_006540, wote=The splicing of exon 11 results original reading frame;
                                                                                                                                       IsoId=015350-7;
                                                                                                                                                              IsoId=015350-6;
                                                                                                                                                                                                                                                  IsoId=015350-4; Sequence=VSP_006542,
                                                                                                                                                                                                                                                                                                                            IsoId=015350-2;
                                                                                                                                                                                                                                                                                                                                                  IsoId=015350-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nda S., Weichselbar
400:792-792(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAY-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shioya H., Ishi
., Weichselbaum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORMS ALPHA AND BETA)
5; PubMed=10391251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6:389-390(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
                                                                                                                                                             Sequence=VSP_006546;
                                                                                                                                                                                    Sequence=VSP_006544, VSP_0065

ng of exon 11 results in a fra

frame. The splicing of exon

the sequence of isoform Alph
                                                                                                                                     Sequence=VSP_006538;
                                                                                                                                                                                                                                                                                                                         Sequence=VSP_006539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91:594-598(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishiko T., Sun X., baum R., Kufe D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishiko T., Sun X., paum R., Kufe D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gu
                                                                                                                                                                                                                                                 VSP_006543
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                                                                                                                                                                                                                                                                                    VSP_006541;
in a frames
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                                                                                                                                                                                      Alpha;
                                                                                                                                                                                                                                                                                     frameshift
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                                                                                   A CENTRAL DNA
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PrODom; PD002681; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
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                                                                                                                                                                                SMART; SM00454; SAM;
                                                                                                                                                                                                                          InterPro; IPR001660;
                                                                                                                                                                                                                                 GO; GO:0003700; F:transcription factor activity; TAS. GO; GO:0008630; P:induction of apoptosis by DNA damage; GO: GO:0006298; P:mismatch repair; TAS. InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                             Genew;
                                                                                                                                              3D-structure.
                                                                                                                                                      Apoptosis; Nuclear
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AF077619;
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Y11416; CAA72221.1;
Y11416; CAA72219.1;
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AAD39696.1;
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                                                                                                                                                      protein;
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                                                                                                                                                      Activator; DNA-binding; Anti-orn; Phosphorylation; Alternative
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       LQRQRVMEAVHFRVRHT IT I PNRGGPGGGPDEWADFGFDLP
                                                         BETA
                                                                  PHOSPHORYLATION
                                                                           DNA-BINDING
                                                                                   POLY-PRO
                                                                                                    POLY-PRO
                                                                                                             MEDIATES OLIGOMERIZATION
                                                                                                                    ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                     TRANSACTIVATION
                                               GNTRCRHWVLCGDRGLSRPVLQGPSG
                                                                          (POTENTIAL).
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Best Local S
Matches 346
                                                                                          Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
--!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROT
                                                                                                                                                                                                                                                                                                                                      Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                           protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein p73 (p53-like transcription factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P73_CERAE
Q9XSK8; Q9TSQ9;
                                                                                                                                                                                                                     TISSUE-Kidney;
                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                           NCBI_TaxID=9534;
(BY SIMILARITY).
SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOT AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
                                                                                                                                                                                                                                                                                                                                                                                                                    OR P73.
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346; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSV-GSSETRGERVIDAVRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMNKLPSVNQLVGQPPPHSSAATPNLGPVGPG----MLNNHGHAVPANGEMSSSHSAQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPMMGTH---MPMAGDMNGLSPTQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--TSIKKRRSPDDELLYLPVRGRETY
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                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                Cercopithecus
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Pred. No. 5.7e-112;
                                                                                                                                                                                                                                            ALPHA
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                      HOMOTYPICALLY
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Best Local S
Matches 340
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EMBL; Y11419;
HSSP; O15350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation;
Apoptosis; Nuclear protein
VARSPLIC 495 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001660; S
Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS: Event-Alternative splicing; Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO THE ABL TYROSINE KINASE SH3 DOMAIN. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOId=Q9XSK8-2; Sequence=VSP_006537;
DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLICOMERIZATION DOMAIN THAT BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a casen the Swiss Institute of Bioinformatics and the EMBL
420
                                                                                                                  306
                                                                                                                                              262
                                                                                                                                                                                                        202
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                                                                                                                                                                                                                                                                                                                                                                                                               340;
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                                                                                                                                                                                                                                                                                                                                                                     LLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPH
                                                                                                                                                                                          GTEFTTVLYNFMCNSSCYGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKAD
                                                                                                                                                                                                                                                   HVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQV
                                                                                                                                                                                                                                                                                                          SFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPPQGAVIRAMPVYKKAE
                                                                                                                                                                                                                                                                                                                                                     GVNKLPSVNQLVGQPPPHSSAATPNLGPVGSG---
                           SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPMMGTH---MPMAGDMNGLSPTQAL
                                                                         EMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMN-
                                                                                                                                  EDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--TSIKKRRSPDDELLYLPVRGRETY
                                                                                                                                                                           GTEFTTILYNFMCNSSCYGGMNRRPILIITLETRDGQVLGRRSFEGRICACPGRDRKAD
                                                                                                                                                                                                                                     HVTDIVKRCPNHELGRDFNEGQSAPASHLIRVEGNNLSQYVDDPVTGRQSVVVPYEPPQV
                                                                                                                                                                                                                                                                                              HFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSAPPPPGTAIRAMPVYKKAE
                                                                                                                 EDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGPGVKKRRHGDEDTYYLQVRGRENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002117; P53.
IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637
                                                                                                                                                                                                                                                                                                                                                                                                             55.4%; ilarity 58.5%; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAA72224.1;
CAA72225.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Activator; DNA-binding; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation: Alternative splicing.
SELTGLGCTNCIEVETSQGLQSIYHLQHITIEDLGALKIPE
GYRMTIWRGLQDLKQGHDYGAAAQQLLRSSNAAAISIGGSG
ELQRQRVMEAVHFRVRHTITLPNRGGFGAGPDEWADRGFDL
PDCKARKQPIKEEFTEAEIH -> RTWGP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1720.5;
Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_006537.
7CB200B919C9C70A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               ..5e-110;
les 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
MLNNHGHAVPANSEMTSSHGTQ--
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                                                                                                                                                                                                                                                                                                                                                                                            PIR; JH0631; JH0631.
HSSP; P04637; lTUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
the Euro
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28-FEB-2003 (Rel. 41, Last
Cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92210006; PubMed=1339362; de Fromentel C.C., Padkel F., Chapus "Rainbow trout p53; cDNA cloning and Gene 112:241-245(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use
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                                                          SEQUENCE
                                                                                                              DOMAIN
                                                                                                                                           DOMAIN
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                               DNA_BIND
                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                             ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
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                                                                                                                                                                                                                                                      Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M75145; AAA49605.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of Apoptosis antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffied and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                 _RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                   DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: Nuclear.
BELONGS TO THE P53 FAMILY.
                                                                                                                                                            Phosphorylation; Apoptosis
TRANSCRIPTION ACTIVATION (ACIDIC).
BY SIMILARITY.
BY SIMILARITY.
OLIGOMERIZATION.
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356
392
318
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                                                                                                                                                                                                                                                                             Transcription regulation; Activator;
                                                 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
8422250765545A1C CRC64;
                                                                                                                                     BASIC (REPRESSION OF DNA-BINDING)
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     839.
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biochemical characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396
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Length 396;
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                                                                                   entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                               between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use by non-profit institutions as long as its con modified and this statement is not removed. Usage b
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;

"Evolutionary conservancy of p53 gene sequences in fish.

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyprinidae; Barbus.
NCBI_TaxID=40830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TP53 OK FOO.
Barbus barbus (Barbel).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinopterygii; Neopterygii;
                                                                                                                                                                                                                                                            FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                     expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                         AF071570;
P04637; 1T
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                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP
                                                                                                  requires a license agreement
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(Rel.
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                                                        AAD34212.1;
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. 40, Last sequ
. 41, Last anno
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Teleostei;
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                                                                                                  (See http://www.isb-sib.ch/announce/
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Ostariophysi; Cypriniformes;
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                                                                                                                               as its content
                                                                                                                                                                                                                                    similarity).
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InterPro;

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Best Local S
Matches 167
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                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDILINE-97344388; PubMed-9200835;

Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,

Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;

"Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence expression during embryogenesis.";

expression during embryogenesis.";
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Submitted
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TP53 OR DRP53.
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                                                                                                                                                                                                         SEQUENCE
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FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes regulared for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
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167; Conser
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28 TRANS
256 BY SI
329 OLIGO
365 BASIC
292 NUCLES
368 PHOSP
                                                                                                                                                                                                                                                  Biotechnol. 6:88-97(1997).
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                                                                                                                                                  the EMBL/GenBank/DDBJ databases
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Pred. No. 4.1e
19; Mismatches
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NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
; OBEZCFZCEA74C304 CRC64;
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BY SIMILARITY
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EMBL; U46693; AAA97408.1;
HSSP; P04637; lTUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-oncogene; DNA-binding;
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SUBUNIT: Binds DNA as a homotetramer (
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
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TRANSCRIPTION ACTIVATION 260 BY SIMILARITY.
                                 40, Last sequence update)
41, Last annotation update)
tigen p53 (Tumor suppressor p53).
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
AC7AB724FA6B61FF CRC64;
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Ictalurus

punctatus (Channel catfish)

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                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Comp. Biochem. Physiol. 120B:675-682(1998).

-i-FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and characterization of the channel catfish (Ictalurus punctatus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99071979; PubMed-9854815;
Luft J.C., Bengten E., Clem L.W., Miller
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein; Phosphorylation; Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00870; P53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
 292
                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                                                156;
                                                                                                                                                                                                                                                                              56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF074967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (So
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                Similarity
ASKKSKNSSSDDEIYTLQVRGKERYEFLKKINDGLELSDVVPPADQEKYRQK 343
                                                                                       LETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQ
                                                                                                                                    VEGNSRAVYQEDGNTQAHSVVVPYEPPQVGSQSTTVLYNYMCNSSCMGGMNRRPILTIIT
                                                                                                                                                                                                        KTCPVLMAVSSSPPPGSVLRATAVYKRSEHVAEVVRRCPHHERSNDSSDGP-APPGHLLR
                                                                                                                                                                                                                              KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR
                                                                                                                                                                                                                                                                                                           SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA
                                MTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ 344
                                                                                                                                                                      VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT
                                                                                                                                                                                                                                                                          SDMLQPQSS--SSPPTSTVPVTSDYPGLLNFTLHFQESSGTKSVTCTYSPDLNKLFCQLA
                                                                  LETQDGHLLGRRTFEVRVCACPGRDRKTEESNFKKQQ-EPKTSGKTLTKRSMKDPPSHPE
                                                                                                                                                                                                                                                                                                                                                                                                                   376
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC26824.1;
                                                                                                                                                                                                                                                                                                                                                                25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                   41989
                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSCRIPTION ACTIVATION (ACIDIC) BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                             Score 795;
                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                 1B89CD98DB3289F2
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                               2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.W., Wilson ... the tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                              ; 88
                                                                                                                                                                                                                                                                                                                                                                             Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p53
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FESSION PROBLEM FOR STORY AND STORY 
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P53_XENLA
P07193;
                                                                                                                                                                                                                                                                                                                               EMBL; S68353; AAC60746.1; -
PIR; A29376; A29376.
HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                   MOD_RES
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                            PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M36962; AAA49923.1; -. EMBL; X05191; CAA28821.1; -. EMBL; X77546; CAA54672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression (By similarity).
-:- SUBUNIT: Binds DNA as a homotetramer (By similarity).
-:- SUBCELLULAR LOCATION: Nuclear.
-:- TISSUE SPECIFICITY: Ubiquitous.
-:- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1988 (Rel. 07, Creat
01-APR-1988 (Rel. 07, Last
28-FEB-2003 (Rel. 41, Last
Cellular tumor antigen p53
                                                                                                                                                                  DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for a protein homologous to human and murine p53., poncogene 1:71-78(1987).
  CONFLICT
                                                                                               DOMAIN
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                              Nuclear protein;
                                                                                                                                                                                                                                    Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in Xenopus laevis embryos.";
Oncogene 9:109-120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata;
Amphibia; Batrachia; Anura; Mesobatrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Overexpression of wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94134403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soussi T., de Fromentel C.C., Mechali M., May P., Kroncloning and characterization of a cDNA from Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88143684; PubMed=2830576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAX antigen expression, or by repression of BCl-2 expression /BV similarity)
  300
344
281
362
52
71
                                                                                                                                                                                                              DNA-binding; Transc
n; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8302570;
t J.H., Wedlich D., Montenarh M., Knoechel W.;
f wild-type p53 interferes with normal development
  267
331
356
293
362
52
71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update) annotation updat
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                                                                                                                                                                                                                                 Transcription regulation;
  MISSING
                   PHOSPHORYLATION (BY SIMILARITY).
T -> S (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                         TRANSCRIPTION ACTIVATION BY SIMILARITY. OLIGOMERIZATION.
                                                                                          BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frog).
                                                                                                                                                                                                              Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suppressor p53).
NI ()
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
  REF.
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opus laevis
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                                                                                                                                                                                                                                      Activator;
                                                                                                                                                                                        (ACIDIC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
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                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene 18:5005-5009(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.; "Nucleotide sequence of the porcine p53 cDNA, and the detection recombinant porcine p53 expressed in vitro with a variety of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
Cellular tumor antiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99422034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                   expression.

SUBUNIT: Binds DNA as a homotetramer (By similarity).

SUBCELLULAR LOCATION: Nuclear.

DISEASE: p53 is found in increased amounts in a wide of transformed cells. p53 is frequently mutated or in
                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scrofa (Pig).
                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                                                                                                                                                          BAX and FAS antigen expression, or by repression
                                                                                                                                                                                                                                                       in many types of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302
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                                            AF098067; AAF04620.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40692 MW;
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Last annotation update)
n p53 (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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Pred. No. 3.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CE1F3E58F020D74D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                          of Bcl-2
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P53_CHICK
ID P53_CHICK
P10360;
P10360;
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Best Local S
Matches 156
"Nucleotide sequence of a CDNA CHICLE ON THE CONTROL OF THE CONTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00/440; ..., Anti-oncogene; DNA-binding; Transcription; Apoptosis.
Nuclear protein; Phosphorylation; Apoptosis.
1 45 TRANSCRIPTION ACTIVATION (ACIDIC)
POMAIN 1 285 BY SIMILARITY.
285 BY SIMILARITY.
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01-MAR-1989 (Rel.
28-FEB-2003 (Rel.
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PRINTS; PR00386; P5301PPRESSR.
ProDom; PD0025881; P53; 2.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                   STRAIN-SPAFAS
                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                          Cellular
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                                                                                                                                                                                             MEDLINE=89083584; PubMed=3060861;
                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                             Archosauria;
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InterPro; IPR002117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 NSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
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                                                                                                                                                                                                                                                                                                                                                                                        tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDALELKD-----AQTARESGENRAHSSHLKSKKG--QSPSRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFLKKGQSCPEPPPGSTKRALPTST---SSSPVQKKKPLDGEYFTLQIRGRERFEMFREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCTTIHYNFMCNSSCMGGMNRRPILTIITLEDASGNLLGRNSFEVRVCACPGRDRRTEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEVVRRCPHHERSSDYSDG-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYEPPEVGS
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(Tumor suppressor
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Pred. No. 4.1e
52; Mismatches
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                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                               Galliformes;
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                                            cell division
                                                                                                                                                        nuclear
                                                          regulation
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Best Local S
Matches 151
                                                                                                                                                                                                    P53_FELCA
P41685;
01-NOV-1995
                                                                                                                                                                                                                                                                                 FELCA
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SEQUENCE
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                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                  TP53 OR TRP53
                                                                                                                                 Cellular
                                                                                                                                                   01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S02193; S02193. HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                          Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13057; CAA31456.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by controlling a set of genes requested the activated genes is an inhibit.

Apoptosis induction seems to be me BAX and FAS antigen expression, or expression (By similarity).

SUBCRIT: Binds DNA as a homotetrar SUBCRILULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                            291 PPTEAPEPPK-KRVLNPDNEIFYLQVRGRRRYEMLKEINEALQLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AAAAPPPLNPP---TPPRAAPSPVVPSTEDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                         tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                        QNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDG--TKRPFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHLIRVEGNPQARYHDDETTKRHSVVVPYEPPEVGSDCTTVLYNFMCNSSCMGGMNRRPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHLIRVEGNSHAQYVEDPITGRQSVLVPYXEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTILTLEGPGGQLLGRRCFEVRVCACPGRDRKIEEENFRK-----RGGAGGVAKRAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YCRLAKPCPVQVRVGVAPPPGSSLRAVAVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002117;
                                                                                                                                              (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation; Apoptosis.

30 TRANSCRIPTION ACTIVATION (ACIDIC).

278 BY SIMILARITY.

339 OLIGOMERIZATION.

364 BASIC (REPRESSION OF DNA-BINDING).

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                            Carnivora;
                                                   Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53.
                                                                                                                         p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₩;
                                                                                                                    annotation update) (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes required for this process. One of an inhibitor of cyclin-dependent kinases. ms to be mediated either by stimulation cression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation; Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 758.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY SIMILARITY). FC37D0FCDF9195B6 CRC64;
                                                   Craniata;
                                                                                                                                                                                                                                                     PRT;
                         Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                     386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 6.1e-45;
cches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions on ong as its content is in no
                         Vertebrata; Euteleostomi;
ia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
                                                                                                                         p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bУ
                                                                                                                                                                                                                                                                                                                                                                                                                          331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  commercia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
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                                                                                                                                                  Query Match
Best Local
                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Lymph node;
MEDLINE-94333960; PubMed-8056458;
Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y.,
Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.;
"Cloning of feline p53 tumor-suppressor gene and it
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                          PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷ <sup>4</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and chromosomal suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94114699; PubMed-8286534;
Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T.,
O'Brien S.J., Tsujimoto H., Hasegawa A.;
                                                                                                                                                                                                                                                                                              Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 34-354 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Int. J. Cancer 58:602-607(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hematopoietic tumors."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                    DNA_BIND
                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                           Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression.

SUBUNIT: Binds DNA as a homotetramer (By similarity).

SUBCELLULAR LOCATION: Nuclear.

DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.

SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAX and FAS antigen expression, or by
                                                                                                                                                                                                                                                                                                                                                                                              D26608; BAA05653.1;
D16460; BAA03927.1;
P04637; 10LG.
                                                                                        al Similarity
147; Conser
                                                             43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Med. Sci. 55:801-805(1993).
     SATWTYSTELKKLYCQIAKTCPIQIKVMTPPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHE
                                DDASGMSAVPAPAAPAPAT----PAPAISWPLSSFVPSQKTYPGAYGFHLGFLQSGTAK
                                                           DHAQNSVTAPSPYAQPSSTFDALSPSPAI-----PSNTDYPGPHSFDVSFQQSSTAK
                                                                                                                                                                                                                                                                                                                                                                                  IPR002117; P53.
                                                                                                                                                 385
285
386 AA;
                                                                                                                                                                                                          94
318
361
304
                                                                                         Conservative
                                                                                                                                                                                                                                                  Phosphorylation; Apoptosis
44 TRANSCRIPTION ACTIVATION
285 BY SIMILARITY
349 OLIGOMERIZATION.
                                                                                                                                                                385
285
                                                                                                                                                                                                        285
349
380
316
                                                                                                                                                  42692
                                                                                                        49.88;
                                                                                                                                                  ¥.
                                                                                         49;
                                                                                                                                                                                                                                                                                                          Transcription regulation; Activator;
                                                                                                                                                              PHOSPHORYLATION (BY SIMILARITY).
K -> R (IN REF. 2).
                                                                                                        Pred.
                                                                                                                   Score 753.5;
                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                      BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                                                                                                                                                          PHOSPHORYLATION
                                                                                                                                                  D08B43BA1BC8EB78 CRC64;
                                                                                         Mismatches
                                                                                                        No. 1.4e-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repression
                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of feline
                                                                                                                                                                                                          (BY
                                                                                                                                                                                                          PRPK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     its aberration
                                                                                                                                                                                                                          DNA-BINDING)
SIGNAL (POTE
                                                                                         Indels
                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Youn H.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Bcl-2
                                                                                                                                                                                                                                                                                (ACIDIC).
                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goitsuka
                                                                                                                      386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor
                                                                                                                                                                                                                         (POTENTIAL).
                                                                                         17;
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in
       154
                                                              94
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SYTCTYSPPLNKLFCQLAKTCPVQLWVRSPPPPGTCVRAMAIYKKSEFMTEVVRRCPHHE

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RESULT 11
P53_TENUD
ID P53_T
AC 09%67
AC 09%67
DT 16-00
DT 16-01
CC Eukar
OC Acthin
OC Acthin
OC Tetra
OX NCB1_
RN [1]
RN [1]
RN [2]
RP SEQUI
RC TISSUE
RC TISSUE
RC TISSUE
RC TISSUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P53_TETMU STANDARL
Q9W679;
16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
28-FEB-2003 (Rel. 41, I
                           DOMAIN
DOMAIN
MOD_RES
                                                                                                           DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon miurus (Congo puffer).

Eukaryota; Metazoa; Chordata; Craniata; Verte
Actinopterygii; Meopterygii; Peleostei; Eute;
Acanthomorpha; Acanthopterygii; Percomorpha;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                    HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Evolutionary conservancy of p53 gene sequences in fish."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bhaskaran A., May D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular tumor antigen
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF071571; AAD34213.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=94908;
                                                                                                                                                          DOMAIN
                                                                                                                                                                                                              Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                    ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Binds DNA as a homotetramer (By SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155
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                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                              PR00386; P53SUPPRESSR
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                                                       86
308
342
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                                                                                                                                                          να-υinding; Transcription regulation; Activator;
Phosphorylation; Apoptosis.
                                                       273
337
363
301
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Last annotatio
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     XX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Tumor suppressor
                        BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                           OLIGOMERIZATION
                                                                                                                                    TRANSCRIPTION ACTIVATION (ACIDIC) BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tyler C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei
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  CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343
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RESULT 12
P53_CANFA
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Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P53_CANFA STANDARD;
Q29537; Q9TV78;
01-NOV-1997 (Rel. 35, Cr
15-DEC-1998 (Rel. 37, La
28-FEB-2003 (Rel. 41, La
Cellular tumor antigen f
                                                   Kraegel S.A., Pazzi K.A., Madewell B.R.;

Sequence analysis of canine p53 in the region of exons 3-8.";

Sequence analysis of canine p53 in the region of exons 3-8.";

Cancer Lett. 92:181-186(1995).

-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
+++
                                                                                                                                                                                                                                                                                              Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka Watari T., Hasagawa A., Tsujimoto H.; "Aberrations of p53 tumor suppressor gene in various spontaneous tumors in the dog.";
                                                                                                                                                                                                                                                                                                                                                                                                   Veldhoen N., Milner J.;
"Isolation of canine p53 cDNA and full length canine p53 protein.";
Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Leukocyte;
MEDLINE=98178696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                         MEDLINE=95323915;
                                                                                                                                                                                                                                     STRAIN-Beagle;
                                                                                                                                                                                                                                                      SEQUENCE OF 25-300 FROM
                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                         TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9615;
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             SUBUNIT: Binds DNA as SUBCELLULAR LOCATION:
                                         expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEVLLGKDPPMGAVLRATATYKKTEHVAEVVRRCPHHQ-----NEDSAEHRSHLIRMEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPPSRDGANSSSPTVPVTTDYPGEYGFKLRFQKSGTAKSVTSTYSETLNKLYCQLAKTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKSKTASSAEEDNNEVYTLQIRGRKRYEMLKKINDGLDLLENKPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERAQYFEHPHTKRQSVTVPYEPPQLGSEFTTILLSFMCNSSCMGGMNRRPILTILTLETQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGIVLGRRCFEVRVCACPGRDRKTEETNSTKMQ:
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is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35, Created)
37, Last sequence update)
41, Last annotation update)
tigen p53 (Tumor suppressor
                                                                                                                                                                                                                          Pubmed-7600529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9519881;
 found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ
'n
                          a homotetramer (By similarity).
             Nuclear.
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increased amounts in a wide variety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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                                                                                                                                                                                                                                                                                    databases
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RESULT 13
P53_BOVIN
ID P53_B
AC Q2962
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Best Local Similarity
Matches 159; Conserv
P53_BOVIN
Q29628;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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HSSP; P04637; 10LG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
                                                                                                    370
                                                                                                                                 351
                                                                                                                                                                                                                                                                             193
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                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                           YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                              VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
                                                                                                    KLMFKREGLDS
                                                                                                                              HLLQKQTSIQS 361
                                                                                                                                                                                                                    LGRNSFEVRVCACPGRDRRTEEENFHKKGEPCPEPPPGSTKRALPPST---SSSPPQKKK
                                                                                                                                                                                                                                             LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                   VSSPPPPNTCVRAMAIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAK
                                                                                                                                                                                                                                                                                                                                                                                                                    TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENNAQTQFSEPQYTNL----GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                          PLDGEYFTLQIRGRERYEMFRNLNEALELKDAQSGKEPGGSRAHSSHLKAKKGQSTSRHK
                                                                                                                                                                                      SPDDELLYLPVRGRETYEMLLKIKESLELMQYLP-----
                                                                                                                                                                                                                                                                                                                                                                                           PL----SSSVPSPKTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLW 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENNVLSSELCPAVDELLLPESVVNWLDE-----DSDDAPRMP--ATSAPTAPGP--APSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002117; P53.
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381 AA;
 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                            STANDARD;
 35, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 744; DB 1;
Pred. No. 6.3e-44;
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l; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEES -> MQEP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY PRPK)
                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761A718FDC93DA59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> P (IN REF.
                            386
                            A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                      -QHT--IETYRQQQQQQQHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                      350
                                                                                                                                                                                                                    309
                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                      240
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                                                                                                                                                                                                                                                                           252
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Bishop R.R.P., Gobright E.E.I.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                          ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 13-386 FROM N.A. SPECIES-Bovine; STRAIN-Holstein; MEDLINE-96401400; PubMed-8807776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dequiedt F., Kettmann R., Burny A., Willems L.; "Nucleotide sequence of the bovine P53 tumor-suppressor cDNA."; DNA Seq. 5:261-264(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat
MOD_RES
                         MOD_RES
                                           DOMAIN
                                                                                    DNA_BIND
                                                                                                 DOMAIN
                                                                                                               Nuclear
                                                                                                                           Anti-oncogene; DNA-binding;
                                                                                                                                                                     PRINTS;
                                                                                                                                                                                      Pfam; PF00870; P53; 1
                                                                                                                                                                                                                 PIR; S51648; S51648.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                      or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=B.indicus; STRAIN=Boran; TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Predominant p53 mutations in enzootic bovine leukemic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES-BOVINE; TISSUE-Liver;
MEDLINE-95352829; PubMed-7626789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos indicus (Zebu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellular tumor antigen p53
                                                                                                                                                                                                  InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Binds DNA as a homotetramer (By similarity) SUBCELLULAR LOCATION: Nuclear. DISEASE: p53 is found in increased amounts in a wide
                                                                                                                                                                                                                                                                                                                                                                                                                                   in
                                                                                                                                                                                                                                                                                                                                                                                                                                               of transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis induction seems to be mediated either by stimulars and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                            X81704; CAA57348.1;
D49825; BAA08629.1;
U74486; AAB51214.1;
                                                                                                                                                                                                                                                                                                                                                                                                                       transformed cells. p53 is frequently mutated or inactivated many types of cancer.
MILARITY: REFORMS TO THE MILARITY:
                                                                                                               protein;
                                                                                                                                                                      PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
385
                           94
318
361
304
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                                                                                                                Phosphorylation;
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                         285
349
380
316
385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Tumor suppressor p53)
                                                                                                                           Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52:53-63(1996).
                                        BASIC (REPRESSION OF NUCLEAR LOCALIZATION
PHOSPHORYLATION
                           PHOSPHORYLATION
                                                                      OLIGOMERIZATION
                                                                                  TRANSCRIPTION BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Thymus
                                                                                                                Apoptosis
                                                      (REPRESSION OF
                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bovine leukemic cell lines.";
                                                                                                 ACTIVATION
(BY
                           (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pecora; Bovoidea;
                            PRPK)
                                        DNA-BINDING)
SIGNAL (POTE
                                                                                                 (ACIDIC).
                            (BY
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                                        (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ULT 14
_MARMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P53_MARMO
036006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                     MEDIINE-9737696; PubMed-9233767;
Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
"Partial characterization of the woodchuck tumor suppressor,
its interaction with woodchuck hepatitis virus X antigen in
                                            ++
                                                                                                                                                                                                                Oncogene 15:327-336(1997)
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                     Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                                                                                                                                               Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
  ÷
                                                                                                                                                                                                                               hepatocarcinogenesis."
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                             FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases, Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
DISEASE: p53 is found in increased amounts in of transformed cells. p53 is frequently mutate in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                      expression SUBUNIT: B:
                                                      SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSLNKLFCQLAKTCPVQLWVDSPPPPGTRVRAMAIYKKLEHMTEVVRRCPHHERSSDYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPGESRAHSSHLKSK----KRPSPSCHKKPMLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRQQQQQQH-QHLLQKQTSIQSPSSYGNSSPPLNK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RALPTNT----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALEL-----KDALDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNRRPILTITLEDSCGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGQSCPEPPPRSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-LAPPOHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELNVEPPLSQETFSDLWNLLPENNLLSSELSAPVDDLLPYTDVATWLDECPNE--APQMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENNAQTQFSEPQYTNLGLL----NSMDQQIQNGSSSTSPYN----TDHAQNSVTAP---
                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
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386 z
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                                                                     Binds DNA as a homotetramer (By
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                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380
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                                                   Nuclear.
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No. 6.5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R -> T (IN REF. 2).
; 222473F28C548F31 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Eut
Sciurognathi; Sciuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                          mutated
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                          wide variety or inactivat
                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                         Sciurinae;
                             inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                        p53,
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-oncogene; DNA-binding; Transc
Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ001022; CAA04478.1; HSSP; P04637; ITUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                         342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                      LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
KGQSTSRHKKIIFKR---EGPDS
                         ROOOQQQHQHLLQKQTSIQSPSS
                                                   SSSPQPKKKPLDGEYFTLKIRGRARFEMFQELNEALELKDAQAEKEPGESRPHPSYLKSK
                                                                                                                 DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNT-----HGI | :|| | | :|| :|| :|| :||
                                                                                                                                                                                SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR
                                                                                                                                                                                                          VQLWVDSTPPPGTRVRAMAIYKKSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGN
                                                                                                                                                                                                                                   IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                                                             AAPSPATSWPLSSSVPSQNTYPGVYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCP
                                                                                                                                                                                                                                                                                                                                        ENNAQTOFSEPOYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDA
                                                                           QMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHT-----IETY
                                                                                                     SGNLLGRNSFEVRVCACPGRDRRTEEENFRKR----
                                                                                                                                                                                                                                                                                                              ENNVLSPVLSPPMDDL-LLSSED--VENWFDK----GPDEALQMSAAPAPKAPTPAASTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                      391
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323
366
309
15
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385
321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          Score 738.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR LOCALIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                     E1DE5DB84BA40182
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
390
                         364
                                                                                                                                                                                                                                                                                                                                                                                .6e-43;
                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVATION
                                                                                                    ----GEPCPEPPPRSTKRALPNGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                             391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                   370
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RESULT 15

P53 ORYLA STANDARD; PRT; 352 AA.

ID P53 ORYLA STANDARD; PRT; 352 AA.

AC P79820; O9PSU7; Q9PSU8;

DT 01-NOV-1997 (Rel. 35, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor F GN TP53 OR P53.

OS Oryzias latipes (Medaka fish) (Japanese riceff OC Eukaryota; Metazoa; Chordata; Craniata; Vertek OC Actinopterygii; Neopterygii; Teleostei; Eutele

suppressor p53). update)

TP53 OR P53.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata
****inonfervdii; Neopterydii; Teleostei; Euteleoste

Euteleostei; Vertebrata;

Euteleostomi; Neoteleostel

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Matches
                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.; "Isolation of CONAs encoding the p53 tumor suppressor gene Japanese Medaka (OTYZ1as latipes)."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Krause M.K., Rhodes L.D., van Beneden R.J.;

*Cloning of the p53 tumor suppressor gene from the Japanese medaka (Oryzias latipes) and evaluation of mutational hotspots in MNNG-exposed fish. *;
                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF003949; AAD01195.1;
EMBL; AF003950; AAD01196.1;
HSSP; P04637; IYCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT THR-91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8090;
[1]
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                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Himedaka;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 189:101-106(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97305153; PubMed-9161419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAX and FAS antigen expression, or by repression of Bc1-2 expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation c
                                                     117 IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN 176
                                                                                                                                                                                                                 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U57306; AAC60146.1; -.
                                                                                                                                                         57 QPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 116
                                                                                                                                                                                                                                            Similarity
IEVRVSKEPPKGAILRATAVYKKTEHVADVVRRCPHHQ-----NEDSVEHRSHLIRVEGS 182
                                                                                                        EPVPTNEVNPPPTTVPVTTDYPGSYELELRFQKSGTAKSVTSTYSETLNKLYCQLAKTSP
                                                                                                                                                                                                                                                                                                                        352 AA;
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                87
302
334
283
351
91
                                                                                                                                                                                                                                                                                                                                           n; Phosphorylation; Apoptosis; Polymorphism.

1 48 TRANSCRIPTION ACTIVATION (ACIDI

2 73 BY SIMILARITY.

2 331 OLIGOMERIZATION.

4 350 BASIC (REPRESSION OF DNA-BINDIN

4 350 BASIC (REPRESSION OF DNA-BINDIN

5 1 PHOSPHORYLATION (BY SIMILARITY)

1 91 S -> T.

2 22 MISSING (IN REF. 1).
                                                                                                                                                                                                                                          23.8%; 52.5%;
                                                                                                                                                                                                                                                                                                                        39753 MW;
                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                  Score 737.5;
                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY SIMILARITY).
S -> T.
                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                   BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                     196868A66351BFF5 CRC64;
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                          No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                          .6e-43;
                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                             Length 352;
                                                                                                                                                                                                               Indels
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288
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                                                                                                                                                 177 SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETR
KRKKSHSSGEEEDNREVFHFEVYGRERYEFLKKINDGLELLE 329
                                KKRRS-----PDDELLYLPVRGRETYEMLLKIKESLELMQ 331
                                                               EGLVLGRRCFEVRICACPGRDRKTEEESRQKTQPK-----KRKVTPNT----SSS
                                                                                               DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSI
                                                                                                                                 QLAQYFEDPYTKRQSVTVPYEPPQPGSEMTTILLSYMCNSSCMGGMNRRPILTILTLET-
                                                                 287
                                                                                                  296
                                                                                                                                   241
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Search completed: August 7, 2003, 09:47:27 Job time: 11.3921 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
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SP_REMBL_23:*

Sp_bacteria

Sp_bacteria

Sp_bacteria

Sp_hugi:*

Sp_invert

SS_invert

SS_inver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
         3104
3108
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3057
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Match Length DB
           BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              830525 seqs, 258052604 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-538-106-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_invertebrate: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_rodent:*
sp_virus:*
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         586
586
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09DEC7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830525
Ogubvý homo sapien
Ogpibá homo sapien
O75080 homo sapien
O89097 mus musculu
O99je2 rattus norv
O93344 homo sapien
O75195 homo sapien
O75195 homo sapien
O9ue10 homo sapien
O9ue10 homo sapien
O9ue10 rattus norv
O9jp6 rattus norv
O9jp6 rattus norv
O9jb6 rattus sapien
O9ue7 gallus gall
O9h3p8 homo sapien
O9up26 homo sapien
O9up26 homo sapien
O9up26 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                            Description
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Smill of need	OBTDY5	4 4	450		1420.5	44
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xenc		13	365	•	1730.5	0
Q9jjp2 mus musculu		11	631	•	1744.5	39
Q8tdy6 homo	o	4	587	•	1746	38
		11	590		1748.5	37
		11	483	•	1766	36
Q9w664 barbus		13	641	•	1777	35
Q99je0 rattus		11	487	•	1802	34
Q99je1 rattus		11	470	58.1	1802	ω
	_	4	487	58.4	1813	32
Q8jhz5 brachydanio		13	457	58.8	1826	31
		11	389	•	1837	30
Q99jd9 rattus norv		11	393	60.2	1868	29
 Q9up74 homo 	Q9UP74	4	356	•	1872	28
075922 homo	075922	4	393	•	1884	27
	Q9NPH7	4	471	٠	2077	26
Q9p1b6 homo	Ø	4	416		2148	25
Q99jd8 rattus		11	55 5	74.8	2323	24
Q99jd7 rattus		11	538	•	2323	23
		11	555	٠	2327	22
Q8jhz6 brachydanio		13	588	•	2330	21
Q8jfe3 brachydanio		13	576	75.5	2344	20
homo	09н3D3	4	555	•	2350	19
Q9p1b7 homo sapien	Q9P1B7	4	516	•	2350	18
Q99jd6 rattus	. Q99JD6	11	461	77.0	2389	17

ALIGNMENTS

	RESULT Q9UBV9	T 1
	58	Q9UBV9 PRELIMINARY; PRT; 586 AA.
	3 2	Ol-MAY-2000 (Treweire) 13 Created)
		(TrEMBLiel. 13,
		(TrEMBLrel. 22, Last annotation
		Homo sapiens (Human).
		Primates; Catarrhini; Hominidae;
		SEQUENCE FROM N.A.
		98448095; P
		Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
		,
		"p63, a p53 homolog at 3q27-29, encodes multiple products with
	R	transactivating, death-inducing, and dominant-negative activities.";
		TO . CETT 2:303-310(1990).
		JENCE FROM N.A.
		Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
		rgoff I.N., Kaufman K.M., Chorzels)
		Jablonska S.;
	RT	"Characterization of an autoantigen associated with chronic ulcerative
•		a member of the
	RL	Invest. Dermatol. 0:0-0(1999).
	RN	
		SEQUENCE FROM N.A.
		Hagiwara K., McMenamin M.G., Harris C.C.;
		Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
		-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
	ය	-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
		EMBL; AF075431; AAC62636.1;
		AAC43038.1;
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RESULT
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Q9P1B4;
01-OCT-2000
01-OCT-2000
01-OCT-2002
P51 isoform
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PROSITE; PS00348; P53; 1.
Nuclear protein
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m delNalpha.
ns (Human).
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InterPro; IPR001217; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRINTS; PR002881; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
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Yokota J
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-i- SUBCELLULAR LOCATION:
-i- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=20388515;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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AF116758;
AF116760;
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AF116763;
AF116764;
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                                         VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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AAF43491.1
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K., Kawahara C.,
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Matches 583; Conserv
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"A second p53 related protein. p73L, with high homology to Blochem. Biophys. Res. Commun. 248:603-607(1998).

-I - SUBCELULIAR LOCATION: NUCLEAR (BY SIMILARITY).

-I - SIMILARITY: BELONGS TO THE P53 FAMILY.

R EMBL; ABD10153; BAA32433.1; --

R HSSP; P04637; 1YCS.

R InterPro; IPR00166; SAM.

R Pfam; PP00870; P53; InterPro; IPR00217; P53.
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075080;
01-NOV-1998
01-NOV-1998
01-OCT-2002
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Nuclear protein.
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Last sequence update)
Last annotation updat
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Pred. No. 4.1e
1; Mismatches
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1.1e-255;
hes 2;
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                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 577
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PRINTS; PR00386; P53SUPPRESSR.
PrODOm; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
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089097;

01-NOV-1998 (Tr

01-NOV-1998 (Tr

01-OCT-2002 (Tr

DN P63 alpha.

TRP63 OR P73H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caput D., McKeon F.; "p63, a p53 homolog at 3g27-29, encodes multiple products with personal material products with a construction and dominant-negative activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98448095; PubMed-9774969;
MEDLINE-98448095; PubMed-9774969;
Kaahad M., Gillett E., Fleming M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1330810; Trp63.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=Thymus:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transactivating, death-inducing, and mol. Cell 2:305-316(1998).
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                                                                                                                                                                                                                                                    al Similarity
577; Conserv
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MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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3 (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                      AA; 65789 MW;
                                                                                                                                                                                                                                                                       98.8<del>8</del>;
98.5<del>8</del>;
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22,
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                     Score 3066; DB 11;
Pred. No. 2.6e-253;
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                                                                                                                                                                                                                                                                                                                                      622E24085B8BDCB7 CRC64;
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Query Match
Best Local S
Matches 575
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Q99JE2;
01-JUN-2001
01-JUN-2001
01-OCT-2002
DN KET alpha
                                                                                                                                                                                                                                                                                                                  P63.

Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata;

Mammalia; Eutheria; Rodentia;

NCBI_TaxID-10116;
                                                                                              SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 586 AA; 65732
                                                                                                                                                          InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
                                                                                                                                       PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1.
                                                                                                                                                                                                                                    FEBS Lett.
                                                                                                                                                                                                                                             variants.";
                                                                                                                                                                                                                                                                 Bamberger C.,
                                                                                                                                                                                                                                                                            MEDLINE=21363378; PubMed=11470269;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-Wistar; TIS
                                                                                                                                                                                                                                                      "Identification and tissue distribution of novel KET/p63
                                                      Local Similarity
wes 575; Conserv
                                                                                                                                                                                         SUBCELLULAR LOCATION: NU SIMILARITY: BELONGS TO SL; AJ277447; CAC37099.1; P; P04637; 1YCS
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nilarity 98.1%;
Conservative
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17,
22,
                                                                                               MW.
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Last sequence update)
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                                                    Score 3057; D
Pred. No. 1.5e
6; Mismatches
                                                      6;
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                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                              78AB8CC4F52BA743 CRC64;
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3 FAMILY.
                                                     1.5e-252;
hes 5;
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                                                                                                                                                                                                                                                                                           Q9H3D4 PRELIMINARY;
Q9H3D4; Q9UP2B;
01-MAR-2001 (TIEMBLIEL 16, C:
01-MAR-2001 (TIEMBLIEL 16, L:
01-MAR-2003 (TIEMBLIEL 23, L:
TA p63 alpha (Tumor protein p
Strausberg R.;
Submitted (NOV-2002) to the iubmitted (NOV-2002) to the i- SUBCELLULAR LOCATION: N -1- SIMILARITY: BELONGS TO EMBL; AF124539; AAG45607.1; EMBL; AF124529; AAG45607.1; EMBL; AF124531; AAG45607.1;
                                                                                                                                                                 Andrews N.C., Caput D., McKeon F.; "p63, a p53 homolog at 3q27-29, encodes multiple produc transactivating, death-inducing, and dominant-negative
                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                   Submitted
                                                                                                                                                           transactivating, death-inc
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=98448095;
                                                                                   TISSUE-Lymph;
                                                                                               SEQUENCE
                                                                                                                           Hagiwara
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                   Yang A.,
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K., M
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Primates;
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TION: NUCLEAR (BY SIMILARITY)
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OR Interpro; IPR002117; P53.

OR Interpro; IPR001660; SAM.

IR Pfam; PF00870; P53; 1.

R PRINTS; PR00386; P53; 1.

R PODOm; PD002681; P53; 1.

R PROSITE; PS00348; P53; 1.

Nuclear Protein.

SEQUENCE 600.
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075195;
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AF124536;
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AF124530;
BC039815;
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                                                              TISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
                                                                                                         PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                        TISEPPRDEWNDENEDMDARRNKOORIKEEGE
                                                                                IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
                                                                                                                                                                                             GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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                                                                                                                                                                                                                                                                                                  PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
                                                                                         IPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQ
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(TrEMBLrel.) (TrEMBLrel.)
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                          PRELIMINARY;
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AAG45607.1;
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AAG625635.1;
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Pred. No. 2.1e-250;
                          PRT;
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Matches 571
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=20388515;
                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                              "Mutation
                                                                                                                                                                                                                                                                                                                                                    rokota
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315
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                                                  195
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PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 641 AA; 72019 MW;
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-1- SIMILARITY: BELONGS TO 1
EMBL; ABD16073; BA332593 1, 1
EMBL; AF116769; AAF43487.1;
EMBL; AF116756; AAF43487.1;
EMBL; AF116757; AAF43487.1;
EMBL; AF116760; AAF43487.1;
EMBL; AF116761; AAF43487.1;
EMBL; AF116762; AAF43487.1;
EMBL; AF116763; AAF43487.1;
EMBL; AF116763; AAF43487.1;
EMBL; AF116765; AAF43487.1;
EMBL; AF116766; AAF43487.1;
EMBL; AF116766; AAF43487.1;
EMBL; AF116766; AAF43487.1;
EMBL; AF116766; AAF43487.1;
EMBL; AF1167676; AAF43487.1;
EMBL; AF116768; AAF43487.1;
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Mammalia; Eutheria; F
NCBI_TaxID=9606;
[1]
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Nat. Med. 4:839-844(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
mEDLINE=98324755; PubMed=9662378;
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; IPR001660; SAM.
00870; P53; 1.
                                                                                                    TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNK
                                  GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                     GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                             PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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K., Kawahara C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primates; Catarrhini; Hominidae;
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99.8%;
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O THE P53 FAMILY.
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Pred. No. 4.2e
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p51, which
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Query Match
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Q9UE10;
01-MAY-2000
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                      -i - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-I - SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL: Y15961; CAA76562.1; -
HSSP; P04637; 1YCS.
InterPro; IPR001617; P53.
InterPro; IPR001617; P53.
InterPro; IPR00160; SAM.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                        Augustin M., Bamberger C., Paul D., Schmale H.; "Cloning and chromosomal mapping of the human p chromosome 3q27 and its murine homolog Ket to m Mamm. Genome 9:899-902(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skeletal muscle, and Keratinocytes; MEDLINE=99018225; PubMed=9799841; Augustin M., Bamberger C., Paul D., Schmal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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les 571; Conser
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                                                                                  TDYPGPHSFDVSEQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                   PYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQXYEDPITGRQSVLV
                                                 PVYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
                                                                                                                                  PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPSSTFDALSPSPAIPSN
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            PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
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                                                                                                                                                                                   Conservative
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Last annotation update)
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                                                                                                                                                                                             Score 3025; DB 4
Pred. No. 1e-249;
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                                                                                                                                                                                   Mismatches
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Ket to mouse
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                                                                                  Query Match
Best Local S
Matches 563
                                                                                                                                                                  MGD; MGI:1330810; Trp63.
InterPro; IPR002117; P53.
InterPro; IPR00160; SAM.
Pfam; PF00870; P53; 1.
PR.NTS; PR00386; P53; 1.
PRODOM; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  088898;
01-NOV-1998
                                                                                                                                  PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 680 AA; 76788
                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TA*p63 alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998
01-OCT-2002
                                                                                                                                                                                                                                                                               -I- SUBCELLULAR LOCATION: NUCLEAR
-I- SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                                                                                      "p63, a p53 homolog at 3g27-29, encodes multiple products
transactivating, death-inducing, and dominant-negative act
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRP63.
                                                                                                                                                                                                                                                                                                                                                    Yang A., Kaghad M., Gillett
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98448095;
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                       ; AF075436;
; P04637; 1)
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                                                                                    563;
            75
                                                                                               Similarity
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                                 PQYTNLGLLNSMDQQIQNGSSGTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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            TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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8 (TrEMBLrel.
8 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                        1YCS
                                                                                                                                                                                                                                                                    AAC62641.1;
                                                                                                                                                                                                                                                                                                                                                                 PubMed=9774969;
                                                                                              96.5%;
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22,
                                                                                                                                   MW;
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                                                                                  Score 2995; DB 11;
Pred. No. 3.7e~247;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                P53
                                                                                                                                   8DFF0284F247C68A CRC64;
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   Query Match
Best Local Similarity
Matches 562; Conserv
                                                                         HSSP; P04637; 1YCS.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PP00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SWART; SW00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q99JE3;
Q99JE3;
01-JUN-2001
01-JUN-2001
01-OCT-2002
TAI KET alph
                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: N
-!- SIMILARITY: BELONGS TO
EMBL; AJ277446; CAC37098.1;
                                                                                                                                                                                                                                                                variants.";
FEBS Lett. 501:121-126(2001).
                                                                                                                                                                                                                                                                                                                           STRAIN-Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269;
                                                                                                                                                                                                                                                                                                               Bamberger C.,
                                                                                                                                                                                                                                                                                                'Identification and
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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    Conservative
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                                                                                                                                                                                                                                                                                                               Schmale
                                                                AA;
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Rodentia;
                                                                                                                                                                                                                                                                                                tissue
                                                                74660 MW;
                   96
96
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17,
22,
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THE P53 FAMILY.
 ; Score 2991; D
; Pred. No. 7.8e
5; Mismatches
                                                                                                                                                                                                                                                                                             distribution
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
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                                                              C953BBAC389D5B70 CRC64;
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DB 11;
1.8e-247;
nes 5;
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RESULT

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AC Q9JJP6

AC Q9

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Q9JJP6;
Q1-OCT-2000
Q1-OCT-2000
Q1-OCT-2002
                            -!- SUBCELLULAR LOCATION: N
-!- SIMILARITY: BELONGS TO
EMBL; Y10258; CAB88216.1; -
HSSP; P04637; IYCS.
                                                                                                         TISSUE-Lingual Schmale H.;
                                                                                                                                                                     Schmale H., Bamberger C.;
"A novel protein with strong
Oncogene 15:1363-1367(1997).
                                                                                                                                                                                                                TISSUE-Lingual epithelium;
MEDLINE=97460723; PubMed=9315105;
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                          TA2 KET alpha.
                                                                                           Submitted
                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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 IPR002117;
IPR001660;
                                                                                           (APR-2000) to
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                                                                                                                                        N.A.
                                                                                                                        epithelium;
P53.
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N: NUCLEAR (BY SIMILARITY)
TO THE P53 FAMILY.
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Best Local Similarity
Matches 562; Conserv
Yasue A.,
"Cloning and
"h. Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; pF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; pD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
Nuclear protein.
SEQUENCE 680 AA; 76760 MW; !
                                                                                                                                                                                                                     Q9DEC7 PR
Q9DEC7;
01-MAR-2001 (T
01-MAR-2001 (T
01-OCT-2002 (T
01-DCT-2002 (T
DN p63 alpha
DNP63A.
Gallus gallus
          SEQUENCE FROM N.A.
MEDLINE-20568966; PubMed=11118893;
MESURINE-20568966; PubMed=11118893;
Yasue A., Tao H., Nohno T., Moriyama
"Cloning and expression of a chick p6
Mech. Dev. 100:105-108(2001).
                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Archosauria; Aves; Neognathae;
                                                                                                                                     NCBI_TaxID=9031;
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98.3%;
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Pred. No. 8.1e-247;
5; Mismatches 5;
                              chick p63
                                                                                                                                                                              Craniata; Vertebrata; Eute; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Best Local Sin
Matches 560;
                                                         O9H3P8 PRELIMINARY;
O9H3P8;
O1-MAR-2001 (TIEMBLIEL . I
O1-MAR-2001 (TIEMBLIEL . I
O1-CTT_2002 (TIEMBLIEL . I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB045224; BAB20631.1; -. HSSP; p04637; 1YCS.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002861; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P55; 1.
Nuclear protein
               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                         Delta N p73L.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                 QIEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSSETR
                                                                                                                                                                                                                                                                          YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV
                                                                                                                                                                        HIEHYSMDDLVSLKIPEQFRHAIWKGILDHRQLHDFSSPPHLLRTPSGASTVSVGSSETR
                                                                                                                                                                                                                                          SQSSYGSNSPPLSKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGTNIPMMGTHMAMTG
                                                                                                                                                                                                                                                  SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                                                             PRELIMINARY;
                          Chordata;
Primates;
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95.68;
                                                           16,
16,
22,
                                                          Created)
Last sequence
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9:
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Pred. No. 2e-244;
                          Craniata; V
Catarrhini;
                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9D1C356B9CCAECE3
                                                           sequence
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                                   Vertebrata; Euteleostomi;
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                            Hominidae;
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InterPro; IPR00160; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOm; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
   Q9P1B5;
Q9P1B5;
01-OCT-2000
01-OCT-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dominant negative isoform, and loss of expression of a guppressor p51-.; suppressor p51-.; submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AB042841; BAB20591.1; -- EMBL; AB042841; BAB20591.1; -- HSSP; P04637; IYCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00348; P53; 1. Nuclear protein.
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                                                                                                                                                                 GERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE 586
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-: SUBCELLULAR LOCATION: NUCLEAR (B.:- SUBLIARITY BELONGS TO THE P53 FEMBL; AF116769; AAF43492.1; JOINED. EMBL; AF116758; AAF43492.1; JOINED. EMBL; AF116769; AAF43492.1; JOINED. EMBL; AF116761; AAF43492.1; JOINED. EMBL; AF116762; AAF43492.1; JOINED. EMBL; AF116762; AAF43492.1; JOINED. EMBL; AF116763; AAF43492.1; JOINED. EMBL; AF116764; AAF43492.1; JOINED. EMBL; AF116765; AAF43492.1; JOINED. EMBL; AF116765; AAF43492.1; JOINED. EMBL; AF116767; AAF43492.1; JOINED. EMBL; 
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PRODOM; PD002681; P53; 1.
PROSTTE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 461 AA; 51305 MW:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DN P63 beta.
P63.
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MEDLINE-98448095; PubMed=9774969;
MEDLINE-98448095, PubMed=9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                            PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PR00318; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hagiwara K., McMenamin M.G., Harris C.C.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                       Pfam; PF00870;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                          Similarity 100.
56; Conservative
                          SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ
SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                  SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
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Metazoa; Chordata; C
Metazoa; Primates; (
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
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AAY43135	ABG95139	ABG95133	AAY05957	ABG95134	ABG95129	ABG95130	AAY50998	AAY05958	ABB74993	ABP61913	AAY50997	AAB11361	ABB74990	ABP61910	ABG95142	ABG95136	ABG95128	AAB82129	AAB11358	AAY05953	AAY45247	ABG95135	ABB74995	ABP61915	ABG95141	AAB11363	AAY05954	ABB74949	ABP61869	AAB11317	AAY41032	AAY05962	ABB74989	ABP61909	AAB11357
p40 prote		oncog	_		oncogene	Human oncogene p51	Rat KET protein.	$\overline{}$	Human p53 homologu	œ.	_	_	Human p53 homologu		oncogene	oncogene	oncogene	prot	- p63 p	cel	_	once	p53	can	O	prot	cell	lung	lung	lung	щ	cell	_	ч	Human p63 protein

ALIGNMENTS

RESULT 1 AAB11362 ID AAB1

AAB11362 standard;

Protein; 461

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30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
WPI; 2000-628399/60
               Wang T,
                                                                      02-APR-1999;
17-DEC-1999;
                                                                                              03-APR-2000; 2000WO-US08896
                                                                                                                             WO200061612-A2.
                                                                                                                                                            Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
vaccine; detection.
                                                                                                                                                                                  Human p63 protein isoform #6.
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2000US-0480884.
2000US-0510376.
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Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein HSP-90; rheumatoid arthritis; cancer; haematopoletic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQHQHLLQKQTSIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQV

LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR YVEDPITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV

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VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK

VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ

180 180 120

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61 61 Query Match Best Local S Matches 461

Similarity

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461;

Conservative

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Score 2450; DB 23; Pred. No. 6.6e-195; Mismatches 0;

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Gaps

MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

60 60 0

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protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemic poletic disorder such as T or B cell lymphoma, chronic myeloid leukaemic poletic disorder such as T or B cell control or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral
                                                                                                                                                                                                                                                                             cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases, involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001; 2001US-272751P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002; 2002WO-US06518
                                                                                                                                                                                                                                                                                                                                                                                                                   proteins (I),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rhabdomyosarcoma; synovial sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CONF-) CONFORMA THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-698710/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetically-defined disease associated with chromosomal ons yielding oncogenic fusion proteins, e.g. cell proliferative, involves administering an inhibitor of heat shock protein 90
    461
                                               This is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 342-344; 389pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 describes a method of treating genetically-defined disease th chromosomal aberrations yielding oncogenic fusion treating cancerous cells containing (I) in a heterogeneous
    ß
                                               the
                                               amino acid
                                           sequence of a human
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                                               oncogenic
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RESULT 3
ABP61914
ID ABP6
XX ABP6
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XX Huma
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XX Homo
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                                                                      The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC activity, and can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC a patient and for treating lung cancer in a patient. Oligonucleotides of CC (I) can be used for detecting the presence of a cancer in a patient, by CC obtaining a biological sample from the patient, contacting the CC biological sample with the oligonucleotide, detecting in the sample, an CC amount of polynucleotide that hybridises to the CC comparing the amount of polynucleotide that hybridises to the CC comparing the amount of polynucleotide that hybridises to the CC plasmaceutical compositions, e.g. vaccines. (I) is useful as a marker to CC plasmaceutical compositions, e.g. vaccines. (I) is useful as a marker to CC indicate the presence or absence of a cancer such as lung cancer.

CC AB092145 to AB092486 and ABP61866 to ABP61992 represent sequences used
                                                        indicate
ABQ92145
in the ex
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-583465/62.
N-PSDB; ABQ92437.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-2000; 2000US-0735705
07-MAY-2001; 2001US-0850716
28-JUN-2001; 2001US-0897778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lung cancer; lung tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McNeill
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D, Watanabe Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Page 333-334; 381pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:343
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RESULT 4
ABB74994
ID 74997
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XX ABB7
XX ABB7
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XX Homo
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Best Local Similarity
Matches 461; Conserv
                                                                                                                                                  28-JUN-2000;
02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
                                        Wang T,
McNeill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lung tumour;
                     TS,
                                                                                                          CORIXA CORP
                  Wang A, Skeiky YAW,
PD, Fanger N, Rette
TS, Carter D, Watan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0685696.
2000US-0735705.
2001US-0850716.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung cancer;
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                  Y YAW, Li SX, Kalos MD, Retter MW, Marnerakis M, Watanabe Y, Peckham DW;
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Pred. No. 6.6e-195;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
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Best Local
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Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 9 HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphona; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, Teali populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL49395 to ABL49300 and ABB74946 to ABB75770 represent sequences used in the exemplification of the present
                                                                                                                                          04-DEC-2002
                                                                                                                                                                                                    ABG95131 standard; Protein; 461
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DB; ABL49251.
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VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ

TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK

120 120 60

YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ

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YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV

181 181 Matches

Similarity

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MLYLENNAQTQFSEPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

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Query Match
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                                                                                                                   oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                             cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell prolif diseases, involves administering an inhibitor of heat shock prot
                                                                                Sequence
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Pred. No. 2.5e-194;
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               The present invention concerns the discovery of a new family of CC cell regulatory proteins (CRPs) termed the p63 family of proteins, CC which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using CC RACE. Sequencing of the amplification product indicated that the CC amplified cDNA possessed a truncated N-terminus, i.e. the CC amplified by screening a cDNA library with a probe corresponding to exons 5-9 of p63. At least 6 different isotypes exist. Splice CC variants differing at the C-terminus are designated as alpha, beta CC and gamma forms, while p63 members differing in the N-terminus are CC designated as deltaN and TA forms, where the deltaN form lacks the CC transactivation domain. The present sequence represents mouse p63 isotype mu-deltaNp63 beta. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent CC activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression CC differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. CC cachexia) and neuronal differentiation and related degenerative concepts.
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N-PSDB; AAX58582.
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15-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse cell regulatory protein
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                                                                                                                                                                                        Cell regulatory protein; p63; hu-deltaNp63 alpha; human; cancer; tumour suppressor; cell cycle control; apoptosis cell proliferation; cell differentiation; therapy.
                                                                                             02-OCT-1998;
                                                                                                                                           WO9919357-A2
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                        Human cell regulatory protein
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                                                                                                                                                                                                                                                                                                                AAY05956 standard;
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                                                         29-MAY-1998;
15-OCT-1997;
                                                                                                                                                                                                                                                                16-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC intron-exon organisation is conserved between p73 and p53, and from CC intron-exon organisation is conserved between p73 and p53, and from CC identify new members of this gene family using a PCR-based strategy CC of amplifying 2 exons in a conserved domain and their intervening CC intron. The human p53 gene was localised to chromosomal position CC 3q27-29. At least 6 different isotypes exist. Splice variants CC differing at the C-terminus have been designated as alpha, beta and CC gamma forms, while p63 members differing in the N-terminus are CC designated as deltaN and TA forms, where the deltaN form lacks the CC transactivation domain. The present sequence represents human CC p63 isotype hu-deltaNp63 alpha, p63 was detected in a variety CC of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes CC and induce apoptosis. Cessation or down-regulation of p63 expression CC differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. CC cachexia) and neuronal differentiation and related degenerative CC disorders. p63 polypeptides (see AAX5957-83) and anti-p63 antibodies of the invention can be used to CC identify compounds useful for treating disorders involving such CC identify compounds useful for treating disorders involving such CC remarkance of an and diagnosis, and in the production of transacric animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 23; Fig 12; 161pp; English
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                                             SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Matches Query Match Best Local

456;

Similarity

100.0%;

Score 2421; DB 23; Pred. No. 2.3e-192; Mismatches

0;

Indels

0;

Gaps

60 0

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RESULT 8
ABG95132
YX ABG9
XX ABG9
XX ABG9
XX Chrc
XX Chrc
KW Proj
KW HSP.
KW Pap.
XX Homm
XX Hom
XX 
                                                                 CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CP 53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC protein isoform in a patient heterozygous for (II). The method is useful
CC protein isoform myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papiliary thyroid
CC arcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 9 HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; AML; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell population, treating proliferative diseases associated with protein or cellular protein isoforms (II) dependent on heat shock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG95132 standard; Protein; 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fritz LC,
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        586 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 331-333; 389pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          describes a method of treating genetically-defined disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            delNalpha
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Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 9. HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG95140
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                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2002
                                                                                                                                                   01-MAR-2001; 2001US-272751P
                                                                                                                                                                           01-MAR-2002; 2002WO-US06518
                                                                                                                                                                                                                         WO200269900-A2
                                                                                                                                                                                                                                               Homo sapiens.
                     Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                             (CONF-) CONFORMA THERAPEUTICS
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                                                                      ABS73332
                                                                                                         Burrows FJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      586
                                                                                                                                   CORP.
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involving administrating HSP90-inhibitor. The method is useful for involving administrating HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion or concept in heterogeneous cell population, treating proliferative disease protein in heterogeneous cell population, treating proliferative disease protein in heterogeneous cell population, treating proliferative disease protein isoform dependent on heat shock protein or cellular protein isoform in a patient heterozygous for (II). The method is useful protein isoform in a patient heterozygous for (II). The method is useful protein isoform chronic myeloid leukaematopoletic disorder such as T or B cell lymphoma, chronic myeloid leukaematopoletic disorder such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 346-348; 389pp;
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Best Local
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                                                                                                                                                                                                                                                               1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                              similarity
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                                                                                                                                                  YVEDPTTGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                           YVEDPITGRQSVLVPYEDPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                    SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPOHTIETYRQQQQQQHQHLILQKQTSIQ
                                                                                                           LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                        LGRRCFEARICACPGRDRKADEDSIRKOQVSDSTKNGDGTKRPFRONTHGIONTSIKKRR
                                    SPSSYGNSSPELNKNNSMNKLPSVSQLINPQQRNALTETTIPDGMGANIPMMGTHMPMAG
                                               SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                         DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIV 456
DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                                                                                                                                                                                                                                                                                                                          586 AA;
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                                                                                                                                                                                                                                                                                                              98.8%;
                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 2.3e-192;
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        456
                                                                                                                                                                                                                                                                                                                            Length 586;
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RESULT 10 AAB11357

AAB11357

standard; Protein;

586

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XXX DEXXXX

21-FEB-2001 AAB11357;

(first entry)

Human p63 protein isoform

#1

cancer;

therapy; treatment;

human;

tumor; immunogenic; cytostatic;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are especially lung cancer, in a patient. Methods described in the invention detection at subsequent time points and comparing the results from the are treated with P2, polynucleotides encoding P2 or antigen presenting development of cancer tells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 243-245; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2000;
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                         361
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                                                                                       241 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGTQMTSIKKRR
                                                                                                                    181 YVEDPITGROSVLVFYEPPQVGTEFTTVLYNFMCNSSCVGGNNRRPILIIVTLETRDGQV
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SPDDELLYLPVRGRETYEMLLKIKESLELMOYLPOHTIETYROOQOOQHOHLLQKQTSIQ
                                              SPDDELLYLPVRGRETYEMLLKIKESLELMOYLPOHTIETYRQOQQQHOHLLQKQTSIQ
                                                                          LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQNTSIKKRR
                                                                                                                               YVEDPITGRQSYLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV 240
                                                                                                                                                             VMTPPPQCAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                          TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK. 120
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990S-0466396.
990S-0476496.
20000S-0480884.
20000S-0510376.
                                                                                                                                                                                                                                                                                                            98.1%;
99.3%;
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Pred. No. 6e-191;
""smatches 2;
                                                                                                                                                                                                                                                                                                                  DB 21; Length 586;
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Qγ

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Query Match Best Local s Matches 453

Similarity

98.1%; 99.3%;

Score 2404; DB 2 Pred. No. 6e-191; 1; Mismatches

23; 1; 2;

Length Indels

0;

Gaps

0,

60

Conservative

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The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC activity, and can be used in gene therapy and in vaccines. Compositions CC apartient and for treating lung cancer in a patient. Oligonucleotides of CC (I) can be used for detecting the presence of a cancer in a patient, by cobtaining a biological sample from the patient, contacting the sample with the oligonucleotide, detecting in the sample, an CC comparing the amount of polynucleotide that hybridises to the oligonucleotide and CC comparing the amount of polynucleotide that hybridises to the oligonucleotide and CC comparing the amount of polynucleotide that hybridises to the oligonucleotide and CC comparing the amount of polynucleotide that hybridises to the oligonucleotide and CC comparing the amount of polynucleotide that hybridises to the oligonucleotide and CC configuration compositions, e.g. vaccines. (I) is useful as a marker to condicate the presence or absence of a cancer such as lung cancer.

CC ABG92145 to ABG92348 and ABG9186 to ABG9192 represent sequences used cin the exemplification of the present invention.
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     Sequence
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McNeill PD,
                                                                                                                                                                                                                                                                                                                   Example 2; Page 326-328;
                                                                                                                                                                                                                                                                                                                                                   by the polynucleotides, vaccines and as markers
                                                                                                                                                                                                                                                                                                                                     Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-2000; 2000US-0735705
07-MAY-2001; 2001US-0850716
28-JUN-2001; 2001US-0897778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang A, Skeik
PD, Fanger N,
D, Watanabe Y,
586 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW, Li SX, Kalos MD, Henders
er N, Retter MW, Durham M, Fanger GR,
be Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lung tumour; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                             381pp; English.
                         present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO:338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TS;
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RESULT 12
ABB74 989
ID ABB74
XX
AC ABB74
XX
AC ABB74
XX
DT 01-MA
XX
Human
XX
Human
XX
Human
XX
Homo
OS Homo
OX
OS Homo
OX
PN WO200
OX
PN W0200
PD 03-Ji
PF 28-JU
PR 21-Ai
PR 21-Ai
PR 21-Ai
PR 12-Di
PR 14-Di
PR 12-Di
PR 1
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                                                                                                                                                                                                                                                                                                                             09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2000;
02-AUG-2000;
21-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                               Wang T,
McNeill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200200174-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human p53 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2002 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB74989 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                          Example 2;
                                                                            Polynucleotides encoding lung lung cancer or stimulating an
                                                                                                                                                                                                                                                                                         (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune
                                                                                                                                            2002-090513/12.
DB; ABL49246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lung tumour;
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                                                                                                                                                                                                                                                                                         CORIXA CORP.
                                                                                                                                                                                                                                              Wang A, Skeiky YAW,
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                                      Page 319-320; 374pp; English
                                                                                                                                                                                                                                                                                                                             2000US-0606421.
2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0662786.
2000US-0685696.
2000US-0735705.
                                                                                                                                                                                                        Fanger N,
Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                      Y YAW, Li SX, Kalos MD, Retter MW, Marnerakis M, Watanabe Y, Peckham DW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p63 (L530S) protein SEQ ID NO:338
                                                                              immune
                                                                                                  tumor polypeptides,
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                                                                              response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunostimulant; vaccine;
                                                                                                    useful
                                                                                                                                                                                                                           Fanger
                                                                                                    for
                                                                                                                                                                                                                           GR;
                                                                                                    treating
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describes

human lung tumour proteins.

Human

Lung

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RESULT 13
AAY105962
ID AAY05
AC AAY05
AC AAY05
AC AAY05
CT 16:AU
DT 16:AU
CT Cell
KW Cell
KW Cell
KW Cell
KW Cell
KW Cell
VX Cell
VX W0991
XX W0991
XX W0991
XX W0991
XX W15-OX
XX 29-MI
PR 15-OX
XX
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Best Local Sim
Matches 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABIA4895 to ABIA4300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                 Cell regulatory protein; p63; mu-deltaNp63 alpha; mouse;
             29-MAY-1998;
15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                   02-OCT-1998;
                                                                                                      WO9919357-A2
                                                                                                                              Mus sp
                                                                                                                                                                                                         Mouse cell
                                                                                                                                                                                                                                      16-AUC-1999
                                                                                                                                                                                                                                                                AAY05962;
                                                                                                                                                                                                                                                                                       AAY05962 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
                                                                                                                                                       proliferation; cell differentiation; there
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFDALSPSPAIPSNTDYPGPHSSDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
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                                                                                                                                                                                                                                                                                                                                                                                                          SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                         regulatory protein
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                                                                                                                                                                                                                                   (first entry)
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A
             98US-0087216.
97US-0062076.
                                                   98WO-US21992
                                                                                                                                                                                                                                                                                       Protein;
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Pred. No. 6e-191;
                                                                                                                                                                                                         p63, isoform
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                                                                                                                                                        therapy
                                                                                                                                                                                                            deltaNp63 alpha
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                                                                                                                                                                   apoptosis;
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(HARD) HARVARD COLLEGE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identified by screening a cDNA library with a probe corresponding to exons 5-9 of p63. At least 6 different isotypes exist. Splice variants differing at the C-terminus are designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltaN and TA forms, where the deltaN form lacks the casingted as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents mouse p63 isotype mu-deltaNp63 alpha. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAY0593-64), polynucleotides (see AAY55972-64) and anti-p63 anti-p64 anti-p65 anti-p67 anti-p67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using RACE. Sequencing of the amplification product indicated that the amplified cDNA possessed a truncated N-terminus, i.e. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated p63 cell regulatory protein for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-277595/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                                                                                                                                    SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
                                                                                                                                                                                                                                                                                                  LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                                                                YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLYLENNAQTQESEPQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                 SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSMQ
                                                                                                                                                                                                                                      {\tt LGRRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRR}
                                                                                                                                                                                                                                                                                                                                                             YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              586 AA;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 20;
1.9e-190;
hes 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 586;
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                           Matches 452;
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18-MAR-1998;
27-JUL-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer. The polypeptides and polynucleotides can be used to stimulate T cells or antigen presenting cells for use in the treatment of lung cancer. The polypeptides and monoclonal antibodies specific for the polypeptides can also be used to inhibit the development of lung cancer. Agents which bind the polypeptides can be used for detecting lung cancer and for monitoring the progression of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides isolated human lung polypeptides. The polypeptides can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lung tumor antigen L503S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated lung tumor polynucleotides, treatment, prevention and monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
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                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                       TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                            MLYLENNAQTQFSEPQYTNLGLLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
     YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                      VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPSSHLIRVEGNSHAQ
                                                                                                          VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                           MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 AA;
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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98US-0040984.
98US-0123912.
98US-0123933.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lung cancer; T cell stimulation
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                                                                                                                                                                                                                                                                                                                                                                                                   97.8%;
99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.3e-190;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used to develop products for the progression of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor nucleic acids and for the treatment of lu
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB11317;
                                           This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynuclectides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient, Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lung cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-628399/60.
N-PSDB; AAC65887.
                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 163-164;
                                                                                                                                                                                                                                                                                                                                                                                      in a
                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide comprising an protein is used for detecting and \boldsymbol{\pi}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPDDELLYLPVRGRETVEMLLKIKESLELMQYLPQHTIETVRQQQQQQQHQHLLIQKQTSIQ
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2000US-0480884.
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61 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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421
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                                                                                                                                     VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPSSHLIRVEGNSHAQ
                                                                                                                                                                               VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
                                                                 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
                                            SPSSYGNSSPPLNKMNSMNKLPSVSQLINDQQRNALTPTTIPDGMGANIPMMGTHMPMAG
                                 SPSSYGNSSPPLNKNNSMNKLPSYSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
DMNGLSPTQALPPPLSMPSTSHCTPPPPPYPTDCSIV
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Pred. No. 2.3e-190;
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Search completed: August Job time : 32.7931 secs 7, 2003, 09:46:27 (OTAZU) XNAJA 30A9 ZIHT

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM protein - protein search, using sw model
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Run on:

ritle:
 perfect score:
 Sequence: US-09-538-106-17 2450 1 MLYLENNAQTQFSEPQYTNL.....HCTPPPPYPTDCSIVRIWQV 461 August 7, 2003, 09:42:54; Search time 12.7172 Seconds (without alignments)
1533.769 Million cell updates/sec

Searched: Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 5.01	sequence 340.	Segmence 340	Sequence	Sequence 341,	Sequence 341,			بر 4	Sequence 19,	Sequence 342,	Sequence		sequence 3337	926 939939	339,	Sequence 339, APP		1	7 7 6	344,	152,	Sequence 152, App		3 1 1 2 1	Sequence Joy App	20	338.	Sequence 338, App	Sequence 343, APP	`	Sequence 343, APP	- 1	Description	

ALIGNMENTS

Qy	망	Оу	Db	Qy	Db	Qy	d dd	Query Maest Low Matches	RESULT 1 US-09-644 US-09-646 ; Sequence ; Patente ; Patente ; APPLII ; APPL
241 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMISIANKK 500		181 YVEDPITGROSVILVPYEPPOVGTEFTTVILVNFMCNSSCVGGMNRRPILITVTLETROGQV 240		121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREENEGQIAPBHLIKVEGNBAAO 180		61 TFDALSPSPAIPSNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120		Watch 100.0%; Score 2450; DB 4; Length 461; Local Similarity 100.0%; Pred. No. 1.2e-216; Local Similarity 0; Mismatches 0; Indels 0; Gaps hes 461; Conservative 0; Mismatches 0; Indels 0; Gaps	2-97-343 2-9343, Application US/09643597 2-9 343, Application US/09643597 2-1 INFORMATION: L INFORMATION: L INFORMATION: CANT: Wang, Tongtong CANT: Honsken, Mancy CANT: Honsken, Mancy CANT: Honsken, Mancy CANT: Li, Samuel X. CANT: Li, Samuel X. CANT: Wang, Aljun CANT: Skeiky, Yasir A.W. CANT: Henderson, Robert A. CAN

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421

APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:

Kalos, Michael D. Wang, Tongt Fan, Liqun

Tongtong

US/09542615A

Bangur, Chaitanya S. Hosken, Nancy A.

GENERAL INFORMATION: Sequence 343, Application Patent No. 6518256 09-542-615A-343 VΩ

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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455CB
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILLING DATE: 2000-04-14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
                     421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV 461
                                                                                                                                                                                      241 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR 300
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                                                                  SPSSYGNGSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                SPSSYGNSSPPLNKMNSNNKLPSYSQLINPQQRNALTPTTIPDGMGANIPMMGTHMFMAG
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APPLICANT: Skeiky, Yasir A.W.
FITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEO ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 461
TYPE: PRT
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Sequence 338, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya
APPLICANT: Hosken, Nancy
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APPLICANT: Hosken, Nancy
APPLICANT: Franger, Gary R.
APPLICANT: Li, Samuel X.
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ative 0;
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Pred. No. 1.2e-216;
"'smatches 0;
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-542-615A-343

Matches 461; Query Match Best Local (

121 61 61 Local

Similarity

100.0%; ilarity 100.0%; Conservative 0

0;

Score 2450; DB 4; Pred. No. 1.2e-216; Mismatches

0;

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361

301 301

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JACHLY, Yasit A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: MCNEILI, PATTICIA D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGROSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Window-
SEQ ID NO 38
LENGTH: 586
TYPE: PP"
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US-09-643-597-338
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US-09-42-615A-338
; Sequence 338, Application US/09542615A
; Patent No. 6518256
; Patent No. 6518250;
; GENERAL INFORMATION:
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                                                        APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
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                                                         Kalos, Michael D.
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Pred. No. 2.9e-212;
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                                APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
NUMBER OF SEQ ID NOS: 358
SEQ ID NO 338
LENGTH: 586
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APPLICANT: Wang, I APPLICANT: Fan, I APPLICANT: Kalos, APPLICANT: Bangun APPLICANT: Hosker APPLICANT: Fange: APPLICANT: Li, SS APPLICANT: SKeik APPLICANT: SKeik

Hosken, Nancy Fanger, Gary R. Li, Samuel X.

Wang, Aijun

AND METHODS FOR THE THERAPY

CANCER

Kalos, Michael D. Bangur, Chaitanya

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Liqun Tongtong

GENERAL INFORMATION:

Sequence 3 patent No.

338, Application US/096064218 o. 6531315

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US-09-542-615A-338
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CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
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ORGANISM: Homo sapiens
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                                                              SPSSYGNSSPPLNKMNSHNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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99.3%;
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Pred. No. 2.9e-21
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; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-643-597-152
                                                  Matches 452;
                                                                Query Match
Best Local
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                                                                                                                                                    APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCMEIL!, Particla D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455011
CURRENT APPLICATION NUMBER: US/09/643,597
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT:
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Li, Samuel X.
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Fan, Ligun
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Hosken, Nancy
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Pred. No. 2.9e-212;
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS OF LUNG CANCER
TITLE OF THENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILLING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 586
TYPE: PRT
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US-09-480-884A-152
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APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael
D.
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                                        VMTPPPOGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV 240
                          VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPSSHLIRVEGNSHAQ
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APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy A.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOI INTEL OF INVENTION: AND DIAGNOSIS OF LUNG CAIFILE REFERENCE: 210121.455C8

CURRENT APPLICATION NUMBER: US/09/542,615A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEG ID NOS: 350

SOFTWARE: FastSEQ for Windows Version 3.0

SEG ID NO 152

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapien
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US-09-542-615A-152
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Best Local S
Matches 452
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                           LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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Fan, Liqun
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99.1%;
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Pred. No. 1.3e-211;
2; Mismatches 2;
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CANCER
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEO ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PAT
ORGANISM: Homo sapien
US-09-606-421B-152
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US-09-606-421B-152
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GENERAL INFORMATION:
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99.1%;
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; SOFTWARE: FastSEQ for Wi
SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-344
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                                                                                                                  RESULT 12
                                                    GENERAL
                                                                 Sequence 344, Application Patent No. 6518256
    APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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Wang, Tongto
Fan, Liqun
Kalos, Mich
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                                                                                                                                                                LSMPSTSHCTPPPPPPTDCSIVRIWQV 516
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Fanger, Gary R.
Li, Samuel X.
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McNeill, Patricia D.
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Fan, Liqun
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                                  Tongtong.
    Michael
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US-09-606-421B-344
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitan
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Cary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A
                                                                                                                                                                                                                                      Sequence 344, Application Patent No. 6531315 GENERAL INFORMATION:
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LENGTH: 516
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.45509
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
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SOFTWARE: FastSEQ for
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; SOFTWARE: FASTSEQ for Wir
; SEQ ID NO 344
; LENCTH: 516 .
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-344
APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI

TITLE OF INVENTION: COMPOSITIONS AND LUNG CANCER

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE REFERENCE: 21021.455(1)

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

CURRENT FILING DATE: 2000-08-21

SOUTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 339

LENGTH: 641

TYPE: PRT

CRGANISM: Homo sapiens

US-09-643-597-339
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Best Local S
Matches 447
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US-09-643-597-339
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Fanger, Gary R.
Li, Samuel X.
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100.0%; Pred. No. 4.8e-210;
tive 0; Mismatches 0;
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RESULT 15
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Best Local Similarity
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APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FO
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA
TITLE REFERENCE: 210121.455C8
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 442;
                                                                                                            TYPE: PRT; ORGANISM: Homo sapiens US-09-542-615A-339
               Qy
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                                                                       tch 95.9%; Score 2350; DB 4; al Similarity 100.0%; Pred. No. 3e-207; al42; Conservative 0; Mismatches 0;
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                                   Wang, Tongtong
Fan, Liqun
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TEGNISHAQYVEDPITGRQSVLV 194	135 PVYKKAEHYTEVVKRCPNHELSREFNEGOTAPPSHLIRVEGNSHAQYVEDDITGROSVLV 194 110	0y 1 Db 1 Qy 1 Db 2 Qy 2 Qy 2 Db 3; Db 3;
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Search completed: August 7, 2003, 09:54:55 Job time: 13.7172 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:
August 7, 2003, 09:46:34; Search time 19.6814 Seconds
(without alignments)
(2781.719 Million cell updates/sec

Title:
US-09-538-106-17
Perfect score: 2450
Sequence:
1 MLYLENNAQTQFSEPQYTNL......HCTPPPPYPTDCSIVRIWQV 461
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 451899 seqs, 118759770 residues
Total number of hits satisfying chosen parameters:

451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: published_Applications_AA:*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_REW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_REW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_REW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
2450 2450 2450 2450 2404 2404 2397 2397 2397 2397 2379 2379 2379 2379	Score
100.0 100.0 100.0 98.1 98.1 97.8 97.8 97.8 97.8 97.1 97.1 97.1	Query Match Length
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9 US-09-735-705-343 10 US-09-850-716A-343 11 US-09-897-778-343 10 US-09-897-778-338 9 US-09-850-716A-338 10 US-09-850-716A-338 10 US-09-850-716A-344 10 US-09-850-716A-344 10 US-09-850-716A-344 10 US-09-850-716A-344 10 US-09-850-716A-349 9 US-09-850-716A-339 10 US-09-850-716A-339	ID ID
Sequence 343, App Sequence 343, App Sequence 338, App Sequence 338, App Sequence 338, App Sequence 152, App Sequence 152, App Sequence 152, App Sequence 152, App Sequence 344, App Sequence 344, App Sequence 344, App Sequence 339, App Sequence 339, App	Description

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955.6669955.66
640 4080 4080 4080 4080 4080 6080 6080 6
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US-09-897-778-339 US-09-735-705-342 US-09-850-716A-342 US-09-857-778-341 US-09-857-716A-341 US-09-857-716A-341 US-09-857-716A-341 US-09-857-716A-340 US-09-857-705-340 US-09-850-716A-340 US-09-850-716A-340 US-09-735-705-340 US-09-735-384-10 US-09-736-695-3 US-09-732-384-3 US-09-732-384-3 US-09-732-384-3 US-09-736-695-3 US-09-736-695-3 US-09-736-695-3 US-09-858-31-36 US-10-160-290-3 US-10-176-691-2 US-10-160-290-3 US-09-968-851-36 US-10-186-473-78 US-10-186-290-3 US-09-968-851-36 US-10-155-059-4 US-09-968-851-36 US-09-968-851-36
Sequence 339, App Sequence 342, App Sequence 342, App Sequence 341, App Sequence 341, App Sequence 341, App Sequence 341, App Sequence 340, App Sequence 30, Appli Sequence 30, Appli Sequence 10, Appli Sequence 20, Appli Sequence 32, Appli Sequence 32, Appli Sequence 34, Appli Sequence 34, Appli Sequence 36, Appli Sequence 4, Appli Sequence 57, Appli Sequence 68, Appli Sequence 78, Appli Sequence 28, Appli Sequence 28, Appli

ALIGNMENTS

Query Match 100.0%; Score 2450; DB 9; Length 401; Best Local Similarity 100.0%; Pred. No. 2.5e-197; Best Local Similarity 100.0%; Pred. No. 2.5e-197; Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 461; Conservative 0; Mismatches 0; Indels 0; Mismatches 0; Mismatche	NCER THI
Gaps (AQPSS	

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APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNEILL, MARCH.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0
LENGTH: 461
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-850-716A-343
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-850-716A-343
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Patent No. US20020115139A1
GENERAL INFORMATION:
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          241 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                       181 YVEDPITGRÓSVLVPYEPPQVGTEFTTVLYNPMCNSSCVGGNNRRPILIIVTLETRDGQV
                                                                              121 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                        121 VMTPPPOGAVIRAMPVYKKAEHVTEVVKRCPNHBLSRBENBGQIAPPSHLIRVBGNSHAQ 180
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                                                                                                                                                                                                      100.0%; Score 2450; DB 10; Length 100.0%; Pred. No. 2.5e-197; rative 0; Mismatches 0; Indels
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Feckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
TYPE: PRT
DECANICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-897-778-343
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 343, Application US/0989
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
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US-09-897-778-343
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                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.0%; Score 2450; DB 10; Similarity 100.0%; Pred. No. 2.5e-197;
                                                         SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQ
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Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 338

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapiens

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           DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 456
                                                               SPSSYGNSSPPLNKMNSMNKLPSYSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Pred. No. 2.6e-193;
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RESULT 6
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                                                       GENERAL INFORMATION:
APPLICANT: Wang, Ton;
APPLICANT: Marnerak:
APPLICANT: Fanger,
APPLICANT: Vedvick,
APPLICANT: Carter, I
APPLICANT: Watanabe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: MCNeill, Patricia
APPLICANT: Retter, Marc W.
                                                                                                                                                             Sequence 338, Application US/09897778 Patent No. US20020147143A1
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                             APPLICANT:
APPLICANT:
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                APPLICANT:
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f: Fanger,
INVENTION:
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Similarity 99.3%;
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                                                                                     Fanger, Gary R. Vedvick, Thomas S.
                                                                        Carter, Darrick
                             Peckham,
                                                          Watanabe, Yoshihiro
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                                          Henderson, Robert A.
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Pred. No. 2.6e
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TITLE

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INVENTION:

COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

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; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,77
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PastSEQ for Windows Version 4.
; SEQ ID NO 338
; LENGTH: 586
; LYPE: PRT
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US-09-735-705-152
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APPLICANT:
APPLICANT:
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo:
SEQ ID NO 152
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Patent No. US
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APPLICANT:
APPLICANT:
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Best Local Similarity
                                    APPLICANT: SKelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Pred. No. 2.6e-193;
1; Mismatches 2;
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; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows V.
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-850-716A-152
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: Sequence 152, Application US/09850716A

: Patent No. US20020115139A1
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Best Local Similarity
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APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
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Pred. No. 1e-192;
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Pred. No. 1e-192;
2; Mismatches
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APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-152
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APPLICANT: Wang, Tonk
APPLICANT: Harnerak
APPLICANT: Fanger,
APPLICANT: Vedvick,
APPLICANT: Carter, I
APPLICANT: Watanabe,
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Best Local Similarity
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                                                                                            Carter, Darrick
Watanabe, Yoshihiro
Henderson, Robert A.
Peckham, David W.
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                                                                                                                                                                                             Conservative
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Pred. No. 1e-192;
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US-09-466-396A-152
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Best Local S
Matches 452
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SEQ ID NO 152
LENGTH: 586
TYPE: PRT
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CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1e-192;
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RESULT 12
US-09-850-716A-344
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US-09-735-705-344
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-344
            Sequence 344, Application US/09850716A Patent No. US20020115139A1
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Patent No. US20020052329A1
GENERAL
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Best Local :
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LENGTH: 516
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CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
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INFORMATION:
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Bangur, Chaitanya;
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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McNeill, Patricia D.
Fanger, Neil
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Pred. No. 2.7e-191;
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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Metter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOPTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-344
APPLICANT: Watanabe, Yoshibiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT ETLING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
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US-09-897-778-344
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APPLICANT: Marner
APPLICANT: Fanger
APPLICANT: Vedvic
APPLICANT: Carter
APPLICANT: Watana
APPLICANT: Hender
APPLICANT: Peckha
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Best Local
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Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                Marnerakis,
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ilarity 100.0%;
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Pred. No. 2.7e-191;
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APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-339
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-344
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APPLICANT:
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SEQ ID NO 344
LENGTH: 516
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Wang, Liqun
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Fanger, Gary R.
Li, Samuel X.
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                                                                                                                                                           Henderson, Robert A. McNeill, Patricia D.
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Skeiky, Yas
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Sequence 339, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Machael D.
APPLICANT: MICHAEL D.
APPLICANTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOUTMARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
ORGANISM: Homo sapiens
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Query Match 34.3%; Score 839.5; DB 1; Best Local Similarity 55.2%; Pred. No. 9.4e-53; Matches 169; Conservative 47; Mismatches 79;	RESULT 1 JH0631 Cellular tumor antigen p53 - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: JH0631 R;de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T. Gene 112, 241-245, 1992 A;Fitle: Rainbow trout p53: cDNA cloning and biochemical characterization. A;Reference number: JH0631; MUID:92210006; PMID:1339362 A;Accession: JH0631 A;Molecule type: mRNA A;Residues: 1-396 <def> A;Cross-references: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829 A;Experimental source: liver C;Comment: This protein is the product of a tumor suppressor gene, p53, whose ina C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; F;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;395/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted</def>	ALIGNMENTS	30 123 5.0 969 2 T15446 31 123 5.0 1572 2 S45251 32 121.5 5.0 947 2 T23107 33 120.5 4.9 901 2 JC6093 34 120 4.9 864 2 T04518 35 120 4.9 864 2 T04518 36 119 4.9 1145 2 T18235 37 119 4.9 1145 2 T32008 38 118.5 4.8 1062 2 G86325 40 118 4.8 1062 2 G86325 41 118 4.8 1586 2 S39580 42 117.5 4.8 596 2 T03908 43 117 4.8 596 2 T03904 44 117 4.8 596 2 T03904 45 116.5 4.8 578 2 T22888
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Oncogene 1, 71-78, 198;
A;Title: Cloning and characterization of a
A;Title: Cloning and characterization of a
                                                                                                                            C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision
C:Accession: S02193
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                                                       A; Title: Nucleotide sequence of a cDNA encoding the chicken A; Reference number: S02193; MUID:89083584; PMID:3060861
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cellular tumor antigen p53 - chicken
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C;Superf
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A;Title: Overexpression of wild-type p53 interferes with A;Reference number: 151639; MUID:94134403; PMID:8302570
A;Accession: S61531
     A;Residues:
                                        A; Accession: S02193
                                                                                       R;Soussi, T.; Begue, A.; Kress, M.;
Nucleic Acids Res. 16, 11383, 1988
                                                                                                                                                                    N; Alternate names: nuclear oncoprotein C; Species: Gallus gallus (chicken)
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A;Accession: S72313
A;Molecule type: mRNA
A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; C;Genetics:
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A; Residues: 1-293,295-363 <HOE>
A; Residues: 1-293,295-363 <HOE>
A; Cross-references: EMBL: X77546; NID: 9468513; PIDN: CAA54672.1; PID: 9468514
R; Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
submitted to the EMBL Data Library, March 1994
                                                                                                            R;Soussi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28821.1; R;Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoeo
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                   Molecule type:
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Keywords: apoptosis; cell division control; DNA binding; homotetramer; nu; Keywords: 3,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
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                                                                                                        D.; May, P.
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-386 <DEGO
A;Cross-references: EMBL:x81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
A;Cross-references: EMBL:x81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
C;Superfamily: cellular tumor antigen p53
C;Superfamily: cellular tumor antigen p53
C;Reywords: apoptoois; cell division control; DNA binding; homotetramer; phc
E;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) *status predicted
E;385/Binding site: phosphoryl-RNA (Ser) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; E;161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predict F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R. submitted to the EMBL Data Library, September 1994 A;Description: Nucleotide sequence of the ovine p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellular tumor antigen p53 - bovine N;Alternate names: tumor-suppressor protein C;Species: Bos primigenius taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-
C;Accession: $51648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S51648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                      PSINKLFCQLAKTCPVQLWVDSPPPPGTRVRAMAIYKKLEHMTEVVRRCPHHERSSDYSD
                                                                                                                                                                                                                                                                                       EPSAPAAPPPAT ----PAPATSWPLSSFVPSQKTYPGNYGFRLGFLQSGTAKSVTCTYS
                                                                                                                                                                                                                                                                                                                       ----SPYAQPSSTEDALSPSPA-------IPSNTDYPGPHSFDVSFQQSSTAKSATWTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPI 227
MNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK
                                                           G-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
                                                                                                       GQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
                                                                                                                                                                                                                           TELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNE
                                                                                                                                                                                                                                                                                                                                                                                                        ELNVEPPLSQETFSDLWNLLPENNLLSSELSAPVDDLLPYTDVATWLDECPNE--APQMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDG--TKRPFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAPPPLNPP--TPPRAAPSPVVPSTEDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENNAQTQFSEPQYTNLGLL----NSMDQQTQNGSSSTSPYN----TDHAQNSVTAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCQIAKTCPIQIKVMTPPPQGAVIRAMPYYKKAEHYTEVVKRCPNHELSREFNEGQIAPP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKL 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 744; DB 1;
Pred. No. 6.5e-46;
5; Mismatches 120;
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A;Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; F;174.177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predict F;390/Binding site: phosphoryi-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA314 R;Hulla, J.E.; Schneider, R.P. Nucleic Acids Res. 21, 713-717, 1993 A;Title: Structure of the rat p53 tumor suppressor gene. A;Reference number: S41149; MUID:93181268; PMID:8441680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Nucleotide sequence of a cDNA encoding the rat p53 A;Reference number: S02192; MUID:89083585; PMID:3060862 A;Accession: S02192
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A;Note: the nucleotide sequence was submitted to the EMBL
C;Genetics:
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A; Residues: 1-173, 'W', 175-391 <HUL>
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A; Residues: 1-391 <SOU>
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    NSSPPLNK---MNSMNKLPSVSQL
                                            FTLKIRGRERFEMFRELNEALELK----
                                                                                  LYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYG
                                                                                                                           VRVCACPGRDRRTEEENFRKKEEHCPELPPGSAKRALPTST----SSSPQQKKKPLDGEY
                                                                                                                                                               ARICACPGRORKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL
                                                                                                                                                                                                         FRHSVVVPYEPPEVGSDYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFE
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41.1%; Pred. No. 2.1e-44;
tive 64; Mismatches 116;
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                                                                                                 MOL. Cell. Biol. 6, 1379-1385, 1986
A;Title: Characterization of the human p53
A:Reference number: A25224; MUID:87064416;
                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000 C;Accession: A25224; A43073; JT0436; S40773; S42669; A22837; A55060; A25397; 4905; I58354; I78850; I52681; S60153
                                                                                                                                                                                                                                                                                                           DNHU53
                                        A; Molecule type: DNA
A; Residues: 1-393 <LAM>
                                                                                A; Reference number: A25224;
A; Accession: A25224
                                                                                                                                                                   R; Lamb,
                                                                                                                                                                                                                                                               cellular tumor antigen p53 [validated] - human
N,Alternate names: cellular phosphoprotein p53
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A;Cross-references: EMBL:X01405; R;Buchman, V.L.; Chumakov, P.M.;
                                                                                                                                                               P.; Crawford,
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A;Title: Tire Com. 17. A;Reference number: JH0633; MUID:9221UUU/; Fi A;Reference number: JH0633 A;Accession: JH0633 A;Accession: JH0633 A;Accession: JH0633 A;Accession: JH0633 A;Accession: JH0633; MUID:9221UUU/; Fi A;Accession: JH0633; MUID:9221UUU/; HI0633; MUID:9221UUU/; HI0633; MUID:9221UUU/; HI0633; MUID:9221UU/; HI0633; MUID:9221UUU/; HI0633; MUID:9221UU/; HI06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuce;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuce;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nuce;Keywords: apoptosis; cellular time.
E;179,182,241,245/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: p53
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R;Legros, Y.; McIntyre, P.
Gene 112, 247-250, 1992
A;Title: The cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellular tumor antigen p53 - golden hamster
N;Alternate names: tumor-suppressor protein p53
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWPLSSS--VPSYKTYQGDYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWV
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LDGEYFTLKIRGQERFKMFQELNEALEL
                                                                                       PDDELLYLPVRGRETYEMLLKIKESLEL 329
                                                                                                                                                                              GRNSFEVRICACPGRDRRTEEKNFQKKGEPCPELPPKSAKRALPTNT---SSSPQPKRKT
                                                                                                                                                                                                                                                                          GRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS
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GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

gene. PMID: 2946935

p53;

oncoprotein p53; transformation suppr

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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-71, 'p', 73-78, 'T', 80-393 <HAR2>
A; Residues: 1-71, 'p', 73-78, 'T', 80-393 <HAR2>
A; Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Mol. Cell. Biol. 6, 4650-4656, 1986
A;Title: Molecular basis for heterogeneity of the human p53 protein.
A;Reference number: A93086; MUID:87089826; PMID:3025664
A;Accession: A25397
                                                                                                                                                                     A; MoLecule type: mRNA; DNA
A; Residues: 66-71, 'p',73-79 <MKI2>
A; Experimental source: clone lambda C113
A; Note: 72-Cys was also found, and appear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;ACCESSION....
A;ACCESSION...
A;MOLECULE type: mRNA
A;Residues: 1-78, 'T',80-393 <HAR1>
A;Residues: 1-78, 'T',80-393 <HAR1>
A;Cross-references: EMBL:M14694; NID:9339813; PIDN:AAA61211.1; PID:g339814
A;Cross-references: clone p53-H-1, transformed hybridoma SV-80 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210 R;Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E. Mol. Cell. Biol. 5, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
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A; Residues: 1-71,'p',73-393 <BUC2>
A; Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476
A; Note: this 72-Pro allele was found in both normal and malignant cell lines
R; Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
submitted to the EMBL Data Library, August 1990
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                                      A; Experimental source:
                                                                                                                                                                                                                                                                                                                  A; Title: Primary structure polymorphism at amino acid residue 72 of human p53 A; Reference number: $42452; MUID:87144273; PMID:3547088 A; Accession: $42452
                                                                                                                                                                                                                                                                                                                                                                                                                 R;Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Mol. Cell. Biol. 7, 961-963, 1987
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A;Molecule type: mRNA
A;Residues: 1-71, 'p',73-272, 'H',274-393 <HAR>
A;Cross-references: GB:KO3199; NID:g189478; PIDN:AAA59989.1; PID:g189479
A;Experimental source: clone pR4-2, cell line A431
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A; Accession: S40773
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A;Note: this 72-Arg allele appears to be about 5 times more
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                                                                                                             A;Molecule type:
                                                                                                                                                   A; Accession:
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R;Matlashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol,
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A; Residues: 1-393 <CHU>
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A; Residues: 1-71,'P',73-393 <ZAK>
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                                                                      66-79 <MKI3>
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       Vousden,
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       K.H.;
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A;Molecule type: mRNA A;Aclecule type: mRNA A;Residues: 1-189, 'LLSIASEWKEICVWSIWMTETLFDIVWWCPMSRLRLALT', 'VPPSTTTTCVTVPAWAA' A;Residues: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433 A;Note: deletion of a C nucleotide causes a frameshift at position 566
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A;Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A;Reference number: I38082; MUID:92007731; PMID:1915267
A;Accession: I38082
                                                     R; Yamada, Y.; Yo
Cancer Res. 51,
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A; Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A; Cross-references: EMBL: X60016; NID: g506444;
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A; Residues: 1-247, 'Q', 249-393 <F06>
A; Cross-references: EMBL: X60015; NID: g506442;
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A; Residues: 1-192, 'R', 194-393 <F02>
A; Cross-references: EMBL:X60011; NID:g506434;
                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453 A;Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 19:R;Futreal, P.A.; Barrett, J.C.; Wiseman, R.W. Nucleic Acids Res. 19, 6977, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-253, 'D', 255-393 <F11>
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A; Residues: 1-212, 'Q', 214-393 <F10>
A; Cross-references: EMBL: X60019; NID:g506450;
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A; Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A; Cross-references: EMBL: X60018; NID: g506448;
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A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                A;Cross-references:
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A; Residues: 1-393 <FUT>
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                                                                                                                                                                                                                                                      A; Title: An Alu polymorphism intragenic to the TP53 gene A; Reference number: I38093; MUID:92107726; PMID:1762941
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A; Residues: 1-247,'Q',249-393 <F08>
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A; Residues: 1-236, 'I', 238-393 <F05>
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A; Residues: 1-245, 'T'
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A; Residues: 1-393 <F03>
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                          p53
gene mutations
number: A44905;
                                                                                      Yoshida,
                                                     ces: EMBL:X54156; NID:g35213; PIDN:CAA38095.1;
oshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J
5800-5805, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,247-393 <F04>
in gastric cancer metastases MUID:92034678; PMID:1933850
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J.; Hirohashi,
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A;Residues: 3-44 <PET>
A;Residues: 3-44 <PET>
R;Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A;Title: Nuclear and nucleolar targeting sequences of c-erb-A,
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A; Residues: 274-277, S', 279-282 <HEN2>
A; Cross-references: GB:S41977; NID:g1679932; PIDN:AAB19325.1;
R; Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A; Title: Alternative splicing of the p53 tumor suppressor general reference number: 152681; MUID:94036762; PMID:8221626
A; Accession: 152681
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 246-247, 'W', 249-250 < YAM>
A; Cross-references: GB: S63157; NID: 9237829; PIDN: AAB20140.1; PID: 9237830
A; Cross-references: GB: S63157; NID: 9237829; PIDN: AB20140.1; PID: 9237830
A; Note: sequence extracted from NCBI backbone (NCBIN: 63157, NCBIP: 63158)
A; Note: mutation from a liver metastasis of a gastric cancer
R; Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 6, 1067-1071, 1991
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A; Residues: 327-331, 'DQTSFQKENC' <CHO>
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                                                                                     SHLKSKKGQSTSRHKKLMFK---TEGPDS
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antigen
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p53
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green monkey
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0; Mismatches 98
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Nucleic Acids Res. 17, 8375, 1989

A;Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosp A;Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosp A;Reference number: $06594

A;Accession: $06594

A;Molecule type: mRNA

A;Residues: 1-393 < RIGS-

A;Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

A;Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

C;Superfamily: cellular tumor antigen p53

C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; F;176,179,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F;392/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390
A; Cross-references: GB:X01237; GB:K01700; NID:953575
A; Cross-references: GB:X01237; GB:K01700; NID:953575
                                                                                                                           Nature 306, 594-597, 1983
A;Title: A single gene and a pseudogene for A;Reference number: A02684; MUID:84068204; FA;Accession: A02684
                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-134, 'V', 136-390 <CHU>
                                                                                                                                                                                                                                                                                                                                                        A;Title: Primary structure of DNA complementary to murine A;Reference number: S06336; MUID:88221682; PMID:3329909 A;Accession: S06336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A22739
A;Molecule type: DNA
A;Residues: 1-134,'V',136-390 <BIE>
A;Cross-references: GB:X00876; NID:g871420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Bienz, B.; Zakut-Houri, R.; Givol, D.; Oren, M. EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular A;Telference number: A22739; MUID:85027173; PMID:6092064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S06594
R;Rigaudy, P.; Eckhart, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Chumakov, P.M. Bloorg. Khim. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Rigaudy, P.; Eckhart, W. Nucleic Acids Res. 17, 8375,
                                                                                                                                                                                                                                           R; Zakut-Houri, R.; Oren, M.;
                                                                                                                                                                                                                                                                                                                             A; Status: not compared with conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: oncoprotein p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellular tumor antigen p53 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1691-1694, 1987
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Pred. No. 5.8e-43;
                                                                                                                                                                                                                                              B.; Lavie, V.; Hazum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                translation
                                                                                                                                                            The cellular PMID:6646235
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A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-47, R:49-78; OW', 82-390 <RES>
A:Cooss-references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
A:Cross-references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
C:Comment: This DNA-binding protein plays an essential role in the regula
C:Comment: The tetramer association region may exhibit a beta-turn, beta-
C:Comment: The tetramer association region may exhibit a beta-turn, beta-
C:Comment: The tetramer association region may exhibit a beta-turn, beta-
C:Comment: The tetramer association region may exhibit a beta-turn, beta-
C:Comment: The tetramer association region may exhibit a beta-turn, beta-
C:Comment: This DNA-binding; homotetramer;
E:1-44/Domain: transcription activation #status predicted <TRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;313-319/Region: nuclear location signal
F;319-357/Region: tetramer association
F;319-357/Region: tetramer association
F;79,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F;173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F;389/Binding site: phosphory1-RNA (Ser) (covalent) #status predicted
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F;114-139/Region: conserved region
F;160-192/Region: L2 loop
F;168-178/Region: conserved region
F;231-252/Region: conserved region
F;233-248/Region: L3 loop
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A; Residues: 1-167, 'G', 169-390 <ARA3>
A; Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1;
R; Jenkins, J.R.; Rudge, K.; Redmond, S.; Wadde Evans, A.
Nucleic Acids Res. 12, 5609-5626, 1984
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R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; submitted to the EMBL Data Library, July 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Cell. Biol. 6, 3434-3439, 1900
A;Title: Immunologically distinct p53 molecules generated by alternative splicing.
A;Reference number: S38822; MUID:87064640; PMID:3023970
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A; Residues: 1-167, 'G', 169-233, 'I', 235-390
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F;99-289/Domain: DNA-binding core #status
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mes 147; Conserv
335 QHTIE-
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                                                                                                    KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
                                                                                                                                                                                                    NSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDST
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                                                                                                                                                                                                                                                                                                                                                                     VMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE-
                                                                                                                                                                                                                                                                                                                                                                                                ATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHEL 155
                                                   LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---
                                                                                                                                                     NSSCMGGMNRRPILTITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPE
                                                                                                                                                                                                                                                          --RCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYEPPEAGSEYTTIHYKYMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.7%; Score 702; DB 1; I
43.2%; Pred. No. 6.8e-43;
tive 54; Mismatches 97;
TYROQOOQHQHLLQKQTSIQS
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A;Gene: p53
C;Superfamily: cellular
C;Keywords: tumor
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A:Title: cDNA cloning and immunological characterization A; Reference number: JC6193; MUID:97208869; PMID:9055811

A:Accession: JC6193
C; Superfamily:
C; Keywords: liv
                                                                                                  A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230 C;Comment: This protein is a multimer, it plays the central role in a comp
                                                                                                                                                                                                                                                                  R;Lee, H.; Larner, J.M.; Hamlin,
Gene 184, 177-183, 1997
                                                                                                                                                                                                                                                                                                                                  tumor suppressor protein p53 - Chinese C; Species: Cricetulus griseus (Chinese C; Date: 11-Apr-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X90592; NID:g1532043; C;Genetics:
                                       A;Gene: p53
                                                             C; Genetics:
                                                                                 iption,
                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-393 <LEE>
                                                                                                                                                                                 A; Accession: JC6176
                                                                                                                                                                                                         A; Reference number: JC6176; A; Contents: liver
                                                                                                                                                                                                                                 A; Title: Cloning and characterization of Chinese hamste
A; Reference number: JC6176; MUID: 97183659; PMID: 9031625
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A; Residues: 1-391 <LEA>
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
JC6193
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Best Local
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                   antigen p53
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Pred. No. 9.5e-43;
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1 09-May-1997
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2;

Length

381;

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F:16-26/Region: conserved region I
F:99-289/Domain: DNA-binding core #status predicted <DBC>
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: conserved region II
F:160-192/Region: conserved region IV
F:231-252/Region: conserved region IV
F:231-252/Region: conserved region V
F:233-248/Region: conserved region V
F:333-348/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7,9,12-18,23-37/Binding site: phosphate (Ser) (covalent) #status predicted
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:312/Binding site: phosphate (Ser) (by cdc2 kinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, Mol. Cell. Biol. 6, 3323-3239, 1986
A;Title: Immunologically distinct p53 molecules generated by alternative spl A;Reference number: S38822; MUID:87064640; PMID:3023970
A;Accession: S38824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cellular tumor antigen p53, minor splice form - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C;Accession: S38824; S35478
                                                                                                                                                                                                                                             C;Superfamily: cellular tumor antigen p53
C;Keywords: alternative splicing; phosphoprotein;
F;1-44/Domain: transcription activation #status p
                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988 C;Comment: This sequence, produced by alternative splicing of the tenth intron, li
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Han, K.A.; Kulesz-Martin, M.F.
Nucleic Acids Res. 20, 1979-1981, 1992
A;Title: Alternatively spliced p53 RNA in transformed and A;Reference number: S35478; MUID:92253421; PMID:1579500
A;Accession: S35478
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A; Residues: 1-381 <HAN>
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A; Residues: 1-381 < ARA>
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Best Local S
Matches 143
                                                                                                                                                                                                                                                                                                     not known
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47.2%; Pre
--+ive 52;
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   submitted to the EMBL Data A; Reference number: Z19114 A; Accession: T19361
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T19361
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C;GenetLos:
A;Gene: p53
A;Introns: 24/1; 61/3
C;Superfamily: cellular tumor a
                                                      R; White, S.
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A; Residues: 1-77 <DEV>
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Best Local Similarity
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Best Local Similarity
Matches 144; Conserv
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                                     Library,
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cellular tumor antigen p53 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
C;Accession: 146226
R;Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Coanticancer Res. 14, 2039-2046, 1994
A;Title: The canine p53 gene is subject to somatic mutations in thypoid card A;Reference number: 146226; MUID:95150524; PMID:7847847
A;Accession: 146226
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                   hypothetical protein C17G1.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T19361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
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                                                                                                                                                                                                                                                                                                                                                                                                KAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEP 198
                                                                                                                                                                                                                                                                                                                                                                     KSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAKYLDDRYTFRHSVVVPYEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSSCYGGMNRRPILIIVTLETRDGQYLGRRCFEARICACPGRDRKADEDSIRKQQYSDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --RCSDGDGLAPPQHLIRVEGNLYPEYLEDRQTFRHSVVVPYEPPBAGSEYTTIHYKYMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SREFNEGO-IAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLXNFMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMCTYSPPLNKLFFQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellular tumor antigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TYRQQQQQQHQHLLQKQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 259.5; DB 2 60.3%; Pred. No. 4.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g508454; PIDN:AAC37327.1;
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Pred. No. 6.1e-42;
6; Mismatches 94
August 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:g508455
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A;Cross-references: GB:M19692; GB:M18402; NID:g158598; PIDN:AAA28934.1; R;HOffmann, F.M.; Fresco, L.D.; Hoffman-Falk, H.; Shilo, B.Z. Cell 35, 393-401, 1983
                                                                                                                                                                                                                                                                                                             protein-tyrosine kinase (EC 2.7.1.112) abl -
C;Species: Drosophila meLanogaster
C;Date: 15-Nov-1984 #sequence_revision 30-Sep
C;Accession: A28128; A00628
                                                                A; Title: Nucleotide sequences of the Drosophila src and A; Reference number: A00628; MUID:84082064; PMID:6317185
                                                                                                                                                                                                                                                                 R;Henkemeyer, M.J.; Bennett, R.L.; Gertler, F.B.; Mol. Cell. Biol. 8, 843-853, 1988
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A; Introns: 40/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-925 <WIL>
A;Cross-references: EMBl
        A;Residues:
                                                  A; Accession:
                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1520 <HEN>
                                                                                                                                                                                                        A;Reference number: A28128;
A;Accession: A28128
                                                                                                                                                                                                                           A; Title: DNA sequence, structure, and tyrosine kinase activity of A; Reference number: A28128; MUID:88174728; PMID:2832740
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Molecule type: DNA Residues: 'A',375,'AQ',378-644,'VGDV'
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Best Local Similarity
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                                                A00628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAEHV---TEVVKRCPNHELSREFNEGQIAPPSHLIRVEG-NSHAQYVEDPITGRQSVLV 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANHMGGMQPMNGTPTEGPTVNNIGLNSNNAAGLPPLSLRSQGPDGSQNNDFPGIPSTSS
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collagen alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL:Z78415; PIDN:CAB01670.1; GSPDB:GN00028; CESP:C17G1.4 se: clone C17G1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPM 418
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1(I) chain; fibrillar collagen carboxyl-terminal homology.
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                                                                                                                                                                                                                                                                                                                                30-Sep-1989
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A;Cross references: FlyBase:FBgn0000017
A;Cross references: 130/1; 310/2; 449/1; 644/3; 735/1; 77
C;Superfamily: Drosophila protein-tyrosine kinase abl;
C;Keywords: ATP; autophosphorylation; phosphoprotein; pr:211-260/Domain: SH3 homology <SH3>
F;211-260/Domain: SH3 homology <SH2>
F;391-363/Domain: Brotein kinase homology <KIN>
F;394-402/Region: protein kinase ATP-binding motif
F;417/Active site: Lys #status predicted
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"Solution structure of a conserved C-terminal domain of
structural homology to the SAM domain.";
EMBO J. 18:4438-4445(1999).
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Kharbanda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 439-506
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Kaelin W.G. Jr.;
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MEDLINE=99318135; PubMed=10391251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2000)
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[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.

INDICTION: NOT INDUCED BY DNA DAWAGE.

DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN.

TO THE ABL TYROSINE KINASE SH3 DOMAIN.

DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN NEUROBLASTOMA AND OLICODENDROGLIOMA.

SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z.-M., U
                                                                                                                                                                                Name=Kappa;
                                                                                                                                                                                                                                                                     Name=Epsilon;
IsoId=O15350-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTS WITH ISOFORM GAMMA, ALPHA, SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HO AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN.
                                                                                                                                                                                                                                                                                                                 Name=Delta
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z.-M., Shioya H., Ishiko T., Sun X., Gu J., E banda S., Weichselbaum R., Kufe D.; are substituted by tyrosine kinase c-abl in the
                                                                                                                                                                                                                         Note=The splicing original reading frame to t
                                                                                                                                                                                                                                                                                                                            Note=The splicing of ex original reading frame;
                                                                                                                                                                  IsoId=015350-7;
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                                                                                                                                                                                                                       Sequence-VSP_006544, VSP_006545;
ng of exon 11 results in a frameshift from
g frame. The splicing of exon 13 reverts the
the sequence of isoform Alpha;
                                                                                                                                                                                                                                                                                                                                           Sequence=VSP_006540, ng of exon 11 results
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement into tremoved. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             VARSPLIC
                                                                                                                                                                                                       PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1.
                                                                                                                                                                                                                        Pfam; PF00870; P53; 1
Pfam; PF00536; SAM; 1
                                                                                                                                                                                                                                                             GO: GO:0003700; F:transcription factor activity; TAS.
GO: GO:0008630; P:induction of apoptosis by DNA damage; TAS
GO: GO:0006298; P:mismatch repair; TAS.
                                                                                                                                                                                                                                                                                                          EMBL; AL136528; CAB927
PDB; 1COK; 17-AUG-99.
PDB; 1DXS; 08-AUG-01.
TRANSFAC; T04931; -.
                                                       VARSPLIC
                                                                                                             DOMAIN
                                                                                                                       DOMAIN
                                                                                                                                                 DOMAIN
                                                                                                                                                           Apoptosis; Nuclear 3D-structure.
                                                                                                                                                                                      PROSITE; PS00348; P53;
                                                                                                                                                                                                                                           InterPro; IPR001660;
                                                                                                                                                                                                                                                                                                Genew; HGNC:12003; TP73.
                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                         MOD_RES
                                                                                   DOMAIN
                                                                                                                                                                             Pranscription regulation;
                                                                                                                                                                                                                                                    InterPro; IPR002117;
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AF077626;
AF077627;
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AF077621;
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AF077616;
AF077617;
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Y11416; CAA72221.
Y11416; CAA72219.
                                                                                                                                                                                                                                                                                                                                                                          AF079090;
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346
168
391
483
131
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                                                                                                                                                                                               SAM;
                                                                                                                                                                                                                                                                                                                                      CAB92742
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                                                                                                                                                                                                                                                                                                                                                                 AAD39696.1;
                                                                                                                                                                   protein;
                            636
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304
435
171
171
171
171
171
194
486
310
                                                       282
                                                                                                                                                                                                                                            SAM.
                                                                                                                                                                    Activator; DNA-binding; Anti-oncogene; phosphorylation; Alternative splicin
                                                                                                                                                                                                                                                                                                                                             JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOINED.
                                                                                                                                                                   Phosphorylation;
     /FTId-VSP_006538.

SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
QYRWTIWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGE
LQRQRVMEAVHERVRHTITIPNRGGPGGGPDEWADFGFDLP
                                                                                          POLY-GLN.
POLY-PRO.
                                                                                                            ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MEDIATES OLIGOMERIZATION (POTENTIAL).
POLY-PRO.
                                                               BETA)
                                                                         PHOSPHORYLATION
                                                                                  DNA-BINDING
                                                                                                                                                 TRANSACTIVATION
                                             isoform Kappa
                                                      GNTRCRHWVLCGDRGLSRPVLQGPSG
                                                                       (POTENTIAL).
TION (BY ABL)
                                                                                                                                                 (BY SIMILARITY).
                                                                         (IN ISOFORM
                                                                                                                                                                   splicing;
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collaboration -

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Query Match
Best Local S
Matches 283
                                                                                                                                                                                                                                                   Caput D.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
-i- WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9XSK8; O9TSQ9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor protein p73 (p53-like transcription factor) (p53-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TP73 OR P73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P73_CERAE
                                                                                                                                                                                                                                                                                                                                                                                                       FISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9534;
                                                                                                                                        (BY SIMILARITY).
SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS
TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HO
AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
                                                       Name-Beta
                                                                                                                         Event-Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               432
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                                                                           IsoId=Q9XSK8-1;
                               IsoId=Q9XSK8-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMNKLPSVSQLIN---PQQRNALTPTTIPDGMGANIPMMGTH---MPMAGDMNGLSPTQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--TSIKKRRSPDDELLYLPVRGRETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTEFTTILYNFMCNSSCVGGMNRRPILIITLEMRDGQVLGRRSFEGRICACPGRDRKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSYDAQSSTFDALSDSPAIPSNTDYPGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPLSMPSTSHCTPPPPPYPTDCSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMNKLPSVNQLVGQPPPHSSAATPNLGPVGPG----MLNNHGHAVPANGEMSSSHSAQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EILMKLKESLELMELVPQPLVDSYRQQQQ-----LLQRPSHLQ-PPSYGPVLSPMNKVHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGRENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAE
       POSSESES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMVSGSHCTPPPPYHADPSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORMS ALPHA AND
  ; Sequence-VSP_006537; an ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.8%;
63.6%;
                                                                         Sequence=Displayed
                                                                                                                       splicing;
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Pred. No. 1.7e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                         Named isoforms=2
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                                                                                                                                                                                                                                                                                                                                                                                                                             BETA).
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JR Pfam; PF00870; P53; 1.

DR Pfam; PF00870; P53; 1.

DR Pfam; PF0036; SAM; 1.

DR PFIDOM; PF0036; P53SUPPRESSR.

DR PRINTS; PR00361; P53; 1.

DR PRINTS; SM0454; SAM; 1.

DR PROSITE; PS00348; P53; 1.

DR PROSITE; PS00348; P53; 1.

DR PROSITE; PS00348; P53; 1.

SR PROSITE; PS00348; P53; 1.

DR PROSITE; PS00348; P53; 1.

DR PROSITE; PS00348; P53; 1.

DR PROSITE; PS01046; P53; 1.

DR PROSITE; PS01046; P53; 1.

DR PROSITE; SM0454; SAM; 1.

DR PROSITE; PS01046; P53; 1.

DR PRINTS; PS01046; P
RESULT 3
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Best Local :
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  P53_ONCMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; 015350; 1COK.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT TO THE ABL TYROSINE KINASE SH3 DOMAIN.
-I- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 LLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPPLSMPSTSHCTPPPPYPTDCSIV
                                                                                                                                                                                                              GVNKLPSVNQLVGQPPPHSSAATPNLGPVGSG----MLNNHGHAVPANSEMTSSHGTQ--
                                                                                                                                                                                                                                                          SMNKLPSVSQLIN--PQQRNALTPTTIPDGMGANIPMMGTH---MPMAGDMNGLSPTQAL
                                                                                                                                                                                                                                                                                                        EILMKLKESLELMELVPQPLVDSYRQQQQ-----LLQRPSHLQ-PPSYGPVLSPMNKVHG
                                                                                                                                                                                                                                                                                                                                                  EMILKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMN-
                                                                                                                                                                                                                                                                                                                                                                                                     EDHYREQQALNESSAKNGAASKRAFKQSPPAVPALGPGVKKRRHGDEDTYYLQVRGRENF
                                                                                                                                                                                                                                                                                                                                                                                                                             EDSIRKQQV--SDSTKNGDGTKRPFRQNTHGIQM--TSIKKRRSPDDELLYLPVRGRETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCPIQIKVSAPPPPGTAIRAMPVYKKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVWTPPPQGAVIRAMPVYKKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt LLSSTMDQMSSRAASASPYTPEHAA-SVPTHSPYAQPSSTFDTMSPAPVIPSNTDYPGPH}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637
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  STANDARD;
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63.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1408.5;
Pred. No. 5.1
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7CB200B919C9C70A CRC64;
                                                                                                                       494
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  396
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.1e-89;
  B
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M75145; AAA49605.1;
PIR; JH0631; JH0631.
HSSP; P04637; lTUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8022;
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P25035;
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWIISS-PROT entry is copyright. It is produced through a collaboration when the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was a superscript of the state of the st
         227
                                                                       180
                                                                                                                                                                                                                                                          107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR00386; P53SUPPRESSR
                                                                                                                                                                                                                          LYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAP
                                                                                                                                                                                                                                                                                                                                                         VTAPSPYAQPS-STFDALS-PSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKK 106
ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQ----VSDSTKNGDGTKRP
                                                                                                                           PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP
                                                                                                                                                                                         LFCQLAKTCPVQIVVDHPPPPGAVVRALAIYKKLSDVADVVRRCPHHQSTSENNEGP-AP
                                                                                                                                                                                                                                                                                                                  VSATEPAPQPSISTLDTGSPPTSTVPTTSDYPGALGFQLRFLQSSTAKSVTCTYSPDLNK
                                                                 RGHLVRVEGNQRSEYMEDGNTLRHSVLVPYEPPQVGSECTTVLYNFMCNSSCMGGMNRRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Apoptosis.
44 TRANSCRIPTION ACTIVATION (ACIDIC)
281 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22,
22,
41,
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356
392
318
395
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
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annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 839.5; DB 1;
Pred. No. 2.2e-50;
- "" matches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (B)
8422250765545A1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                         179
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Query Match
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Matches 167
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P53_BARBU
Q9W678;
16-OCT-2001
                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.; "Evolutionary conservancy of p53 gene sequences in fish."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                         SEQUENCE
                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                            EMBL; AF071570;
HSSP; P04637; 1
                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bhaskaran A., May D., Rand-We
"Evolutionary conservancy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinopterygii; Neopterygii; Cyprinidae; Barbus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last
28-FEB-2003 (Rel. 41, Last
Cellular tumor antigen p53
                                                                                    DOMAIN
                                                                                                    DOMAIN
                                                                                                                               DNA_BIND
                                                                                                                                             DOMAIN
                                                                                                                                                        Nuclear protein;
                                                                                                                                                                          Anti-oncogene; DNA-binding;
                                                                                                                                                                                       ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                   Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=40830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbus barbus (Barbel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).

SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339
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                                                                                                                                                                                                                  PR00386; P53SUPPRESSR.
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                                                                                                                                                                                                                                               637; 1TUP.
IPR002117;
                                                         369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                           AAD34212.1; -.
                                                                                                             Phosphorylation; Apoptosis
28 TRANSCRIPTION ACTIVATION
256 BY SIMILARITY.
329 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40, Created)
40, Last sequence update)
41, Last annotation updat
                                                                                    256
329
365
292
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                                                                                                                                                                                                                                                P53.
             33.4%;
                                                         WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Tumor
                                                                                                                                                                       Transcription regulation; Activator;
                                                                      BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Craniata;
Teleostei;
                           Score 819.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                         OBE2CF2CEA74C304 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ⋧
                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p53).
                            Length 369;
                                                                                                                                             (ACIDIC).
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Similarity

Conservative

49;

Pred. No. 4.6e-49

Mismatches

87;

23;

Gaps

8

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RESULT
P53_BRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-97344388; PubMed-9200835;

Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford of Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford of Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;

"Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA expression during embryogenesis.";

"An Mar. Biol. Biotechnol. 6:88-97(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P53_BRARE STANDARD; PRT; 373 AA. P79734; Q90440; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor | TP53 OR DRP53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
                                                                           modified
                                                                                                                                                                                                                                                                                                                                                                                                                           Winge
                              s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in lifted and this statement is not removed. Usage by and for comities requires a license agreement (See http://www.isb-sib.ch/ansend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                 FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                               expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLKKINDSLELSDVVPPSEMDRYRQK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQVSDSTKNGD----GTKRPF-RQNTHGIQMTSIKKRR----SPDDELLYLPVRGRETYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLYNFMCNSSCMGGMNRRPILTIISLETHDGQLLGRRSFEVRVCACPGRDRKTEESNFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRCPHHERTPD-GDG-LAPAAHLIRVEGNSRALYREDDVNSRHSVVVPYEVPQLGSEFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMVVNVAPPQGSVIRATAIYKKSEHVAEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELINDEYLPSSFDPNIFDNVLTEQPQPSTSP-----PTASVPVATDYPGEHGFKLGF
                                                                                                                                                                                                                                                                                                                                                                                                        (JAN-1996) to the EMBL/GenBank/DDBJ databases
AAB40617.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h) (Danio rerio).
a; Craniata; Verte
; Teleostei; Osta
                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
                                                                                                                                                                                                                    similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p53).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                             a collaboration
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RESULT 6
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Best Local S
Matches 171
                                                                                                                                                                                                                                                                                                                 P53_ICTPU
093379;
16-OCT-2001
                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND
DOMAIN
DOMAIN
MEDIINE-99071979; PubMed-9854815;
Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
"Identification and characterization of the tumor suppressor p53 in channel catfish (Ictalurus punctatus).";
Comp. Biochem. Physiol. 120B:675-682(1998).
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
MOD_RES
                                                                                                                                                                                                     ICLAIURUS punctatus (Channel catfish).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002117;
Pfam; PF00870; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P04637; 1TUP.
ZFIN; ZDB-GENE-990415-270;
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00386; P53SUPPRESSR.
                                                                                                                                                                                               Ictaluridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; Phosphorylation; Apoptos:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                         286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 TCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QNDSQ-EFAELWEKNLIIQPPGGGSCWDIIN--DEEYLPGS-----FDPNFFEN-VLEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ENNAQTQFSEPQYTNL------GLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGNSHAQYYEDPITGRQSYLVPYEPPQVGTEFTTYLYNFMCNSSCVGGMNRRPILIIVTL
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Pred.
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BASIC (REPRESSION OF DNA-BINDING)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSCRIPTION ACTIVATION
                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                              Ostariophysi;
                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                      p53).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                      _XENLA
P53_XENLA
P07193;
01-APR-1988
Xenopodinae; Xeno
NCBI_TaxID=8355;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SW:
between
                                  Eukaryota; Metazoa; Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use
                                                                    Xenopus laevis (African clawed frog)
                                                                                               Cellular
                                                                                                           01-APR-1988
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                          114
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                                                                                                                                                                                                                                                                                                                                                                             173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opean Bloinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way dand this statement is not removed. Usage by and for commercial is requires a license agreement (See http://www.isb-slb.ch/announce/an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                         LETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQ
                                                                                                                                                                                                                                      ASKKSKNSSSDDEIYTLQVRGKERYEFLKKINDGLELSDVVPPADQEKYRQK 343
                                                                                                                                                                                                                                                                                                                                                                             VEGNSHAQYVEDPITGROSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVT
                                                                                                                                                                                                                                                                                                                                                                                                       KTCPVLMAVSSSPPPGSVLRATAVYKRSEHVAEVVRRCPHHERSNDSSDGP-APPGHLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIA 112
                                                                                                                                                                                                                                                                                         LETQDGHLLGRRTFEVRVCACPGRDRKTEESNFKKQQ-EPKTSGKTLTKRSMKDPPSHPE
                                                                                                                                                                                                                                                                                                                                                 VEGNSRAVYQEDGNTQAHSVVVPYEPPQVGSQSTTVLYNYMCNSSCMGGMNRRPILTIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                  KTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDMLQPQSS---SSPPTSTVPVTSDYPGLLNFTLHFQESSGTKSVTCTYSPDLNKLFCQLA
                                                       Metazoa; Chordata;
                                                                                                           3 (Rel. 07, 8 (Rel. 07, 8 (Rel. 41, 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376
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                          Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ä,
                                                                                              antigen
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41989
                                          Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.4%;
                                                                                                           Last sequence update)
Last annotation updat
                                                                                              p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is an inhibitor of cyclin-dependent kinases. seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
                                                                                               (Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Activator;
                                        Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 795; DB 1;
Pred. No. 2.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION ACTIVATION (ACIDIC). BY SIMILARITY. OLIGOMERIZATION.
                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1B89CD98DB3289F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                            tion update)
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                                                                                                                                                                                                                                                                                                                                                                                                                  p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                          Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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Best Local S
Matches 151
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-94134403; PubMed-8302570;
Hoever M., Clement J.H., Wedlich D., Montenarh M., Knoechel W.;
"Overexpression of wild-type p53 interferes with normal development
in Xenopus laevis embryos.";
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                        Nuclear
                                                                                                                                                                                                                                                                                                                                                     Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A29376; A29376.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The sympactic institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in Xenopus laevis embryos.
Oncogene 9:109-120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for a protein homologous to human and murine p53. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soussi T., de Fromentel C.C., Mechali M., May P., Kro
Cloning and characterization of a cDNA from Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=88143684; PubMed=2830576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                      Loca1 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              , M36962; AAA49923.1; X05191; CAA28821.1; X77546; CAA54672.1; S68353; AAC60746.1;
            188
                                        128
                                                                                           68
                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                              PR00386; P53SUPPRESSR.
GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFE
                                      GSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYMEDVNS
                                                       GAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT
                                                                                           SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVESPPPR
                                                                                                           SPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002117; P53.
                                                                                                                                                                                                    296
363
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                Phosphorylation; Apoptosis.
29 TRANSCRIPTION ACTIVATION
267 BY SIMILARITY.
331 OLIGOMERIZATION.
                                                                                                                                                                                                                                267
331
356
293
362
71
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                                                                                                                                                            31.1%; 54.5%;
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                                                                                                                                                                                                       MW;
                                                                                                                                                 42;
                                                                                                                                                Score 762; DB
Pred. No. 3.9e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Transcription regulation;
                                                                                                                                                                                                     MISSING (IN REF. 2)
MISSING (IN REF. 2)
CE1F3E58F020D74D
                                                                                                                                                                                                                                           PHOSPHORYLATION (BY SIMILARITY).
T -> S (IN REF. 2).
                                                                                                                                                                                                                                                                      BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions ng as its content is in
                                                                                                                                                DB 1; I
8.9e-45;
les 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                         Length 363;
                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kress
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laevis coding
                                                                                                                                                                                                                                                                                                                            (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                     Activator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
MBL outstation -
                                                                                                                                                 16;
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                                                                                                                                                Gaps
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RESULT 8
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                           use
                                                                                                                                                                                                                    EMBL; AF098067; AAF04620.1; HSSP; P04637; 1C26.
                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                       Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene 18:5005-5009(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant antibodies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99422034; PubMed=10490836; Burr P.D., Argyle D.J., Reid S.W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9TUB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P53_PIG
 MOD_RES
                                                                                                                                              ProDom; PD002681; P53; 2. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                    HSSP; P04637; 1C26.
InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001
28-FEB-2003
                                                                                                                                                                         PRINTS; PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jurr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
Nucleotide sequence of the porcine p53 cDNA, and the detection
recombinant_porcine p53 expressed in vitro with a variety of ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                       European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                             in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: p53 is found in
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Binds DNA as a homotetramer (By similarity). SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAX and FAS antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis induction
                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
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                                                                                                                                                                                                                                                                                                                                                                                                         transformed cells. p53 is frequently
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1 (Rel. 40, Last s
3 (Rel. 41, Last s
 385
                                                                                                                               DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
annotation update)
(Tumor suppressor
                                                                                                                             Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                         increased amounts in
                                        BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
                            PHOSPHORYLATION
                                                                        OLIGOMERIZATION
                                                                                      BY SIMILARITY.
                                                                                                TRANSCRIPTION ACTIVATION (ACIDIC)
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                                                                                                                 Apoptosis
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                           or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                       wide variety
                                                                                                                             Activator,
                                        (POTENTIAL).
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of anti-p53
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  use by non-profit institutions as long a modified and this statement is not removed; entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 16:11383-11383(1988).

-I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restricted the succession of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellular tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Creat
01-MAR-1989 (Rel. 10, Last
28-FEB-2003 (Rel. 41, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archosauria; Aves;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oncoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soussi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89083584; PubMed=3060861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPAFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of a cDNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loca 1
                                                                                                                                                                                                           BAX and FAS antigen expression, or by repression of B expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKI
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45.3%; Pred. No. 4.
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                                                                              There are no restrictions on ong as its content is in no
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RESULT 10
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P41685;
01-NOV-1995 (Rel. 32, Cr
01-NOV-1995 (Rel. 32, La
28-FEB-2003 (Rel. 41, La
Cellular tumor antigen p
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PRODOM; PD002681; P53;
PROSITE; PS00348; P53;
                                            SEQUENCE OF 34-354 FROM N.A.
MEDLINE-94114699; PubMed-8286534;
Okuda M., Uneda A., Matsumoto Y., Momoi Y., Watari T.,
O'Brien S.J., Tsujimoto H., Hasegawa A.;
suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                         Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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MOD_RES
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PIR; S02193; S02193.
HSSP; P04637; 1TUP.
                                                                                                                                                                                          Watari T., Goitsuka R., Tsujimoto H., Hasegawa A. "Cloning of feline p53 tumor-suppressor gene and hematopoietic tumors.";
                                                                                                                                                                                                                                                              Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y.,
                                                                                                                                                                                                                                                                                  MEDLINE=94333960; PubMed=8056458;
                                                                                                                                                                                                                                                                                                             TISSUE=Lymph node;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9685
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
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30 TRANSCRIPTION ACTIVATION (ACIDIC).
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation update) (Tumor suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 758.5; DB 1
Pred. No. 6.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY. OLIGOMERIZATION.
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Felis.
                        p53 tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Vet. Med. Sci. 55:801-805(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D26608; BAA05653.1;
EMBL; D16460; BAA03927.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (Sèe http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION:
DISEASE: p53 is found
of transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Acts as a tumor suppressor in many tumor types; induce growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation a a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Bi
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                                                                                                                                                                                                                                                              155
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292
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                                                                                                                                                                                                                                                                                                                                                                  95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
PPPGSTKRALPPST---SSTPPQKKKPLDGEYFTLQIRGRERFEMFRELNEALEL
                             KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLEL
                                                                                                                                                                                                                                    NSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDST
                                                                                                                                                                                                                                                                                                                 SVTCTYSPPLNKLFCQLAKTCPVQLWVRSPPPPGTCVRAMAIYKKSEFMTEVVRRCPHHE
                                                                                                                                                                                                                                                                                                                                                                  SATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHE
                                                                                                                                                                                                                                                                                                                                                                                                                     DDASGMSAVPAPAAPAPAT----PAPAISWPLSSFVPSQKTYPGAYGFHLGFLQSGTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DHAQNSVTAPSPYAQPSSTFDALSPSPAI ------
                                                                                                        NSSCMGGMNRRPIITIITLEDSNGKLLGRNSFEVRVCAC PGRDRRTEEENFRKKGEPCPE
                                                                                                                                                                                                           RCPDSSDG-LAPPQHLIRVEGNLHAKYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNFMC
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386 1
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44 TRANSCRIPTION ACTIVATION
285 BY SIMILARITY.
349 OLIGOMERIZATION.
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285
42692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s found in increased amounts in a wide variety cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 753.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
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D08B43BA1BC8EB78
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DOMAIN
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Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
-I-FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.

Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00870; P53; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TP53 OR P53
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bhaskaran A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon miurus (Congo puffer)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETMU
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                                                                                                                                                                                                                                                       QPSSTEDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP
                                              SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR
                                                                                                                                     IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                    EPPSRDGANSSSPTVPVTTDYPGEYGFKLRFQKSGTAKSVTSTYSEILNKLYCQLAKTSL
ERAQYFEHPHTKRQSVTVPYEPPQLGSEFTTILLSFMCNSSCMGGMNRRPILTILTLETQ
                                                                                                           VEVLLGKDPPMGAVLRATATYKKTEHVAEVVRRCPHHQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation; Apoptosis.

TRANSCRIPTION ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    41266 MW;
                                                                                                                                                                                                                                                                                                                                                               30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rand-Weaver M., Tyler C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                            Pred. No. 5.7e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Score 745;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (B)
ACC10EEE2F5F9CFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
                                                                                                                                                                                                                                                                                                                                                               DB 1;
.7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                  76;
                                                                                                                                                                                                                                                                                                                                                                                    Length 367;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                           NEDSAEHRSHLIRMEGS
                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                               Gaps
                                                    236
                                                                                                                                                             176
                                                                                                                                                                                                                    126
                                                                                                        181
241
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RESULT 12
P53_CAMP
ID P53_CA
ID P53_CA
ID P53_CA
ID P53_CA
ID P53_CA
ID Q2953
IT Q1-DE
ID 15-DE
ID 17-DE
ID 17-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P53_CANFA STANDARD; P1
Q29537; Q9TV78;
01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last seque
28-FEB-2003 (Rel. 41, Last annot
Cellular tumor antigen p53 (Tumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tiros (n. ....
Carais familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Cranidae; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kraegel S.A., Pazzi K.A., Madewell B.R., "Sequence analysis of canine p53 in the Cancer Lett. 92:181-186(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-yollow Veldheen N., Milner J., Veldheen N., Milner J., "Isolation of canine p53 cDNA and "Isolation canine p53 protein.",
                                                                                                                                or send an
                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Beagle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 25-300 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Setoguchi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Leukocyte;
MEDLINE-98178696; PubMed-9519881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95323915; PubMed=7600529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watari T., Hasagawa A., Ts
"Aberrations of p53 tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                               expression.
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                     in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
AF060514; AAC16909.1; -. AB020761; BAA78379.1; -. S77819; AAB42022.1; -. P04637; 10LG.
                                                                                                                                and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                    non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKSKTASSAEEDNNEVYTLQIRGRKRYEMLKKINDGLDLLENKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGIVLGRRCFEVRVCACPGRDRKTEETNSTKMQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DEC-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sakai T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsujimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okuda M., Minehata K., Yazawa M., Ishizaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      suppressor gene in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation updat
(Tumor suppresso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the region of exons 3-8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          381
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                                                                                                                                                                                                                  as its content
                                                                                                                                                          http://www.isb-sib.ch/announce/
                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    databases
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                                                                                                                                                                                                                                                                       EMBL outstation
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RESULT
P53_B95V
ID P50
AC Q2
DT Q1
DT Q1
OT Q1
OT Q1
OS B COC F COC F 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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Q29628;
Q1-NOV-1997
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CONFLICT
SEQUENCE
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ProDom;
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                                Dequiedt F.,
"Nucleotide
                                                              MEDLINE=95352829; PubMed=7626789; Dequiedt F., Kettmann R., Burny A
                                                                                                                                                                                                                                                                                   Bos indicus (2ebu).
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cellular tumor antigen p53
                                                                                                                               SPECIES-Bovine;
                                                                                                                                                                                                                           NCBI_TaxID=9913,
                                                                                                                                                                                                                                                            Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
28-FEB-2003
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                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  taurus (Bovine), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLDGEYFTLQIRGRERYEMFRNLNEALELKDAQSGKEPGGSRAHSSHLKAKKGQSTSRHK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSSPPPPNTCVRAMAIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENNAQTQFSEPQYTNL----GLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLMFKREGLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENNVLSSELCPAVDELLLPESVVNWLDE-----DSDDAPRMP--ATSAPTAPGP--APSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGRNSFEVRVCACPGRDRRTEEENFHKKGEPCPEPPPGSTKRALPPST---SSSPPQKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 (Rel. 35,
7 (Rel. 35,
8 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA;
                                , Kettmann R.
sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                               TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSVPSPKTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLW 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NA-binding; Transcription regulation; Activator; Phosphorylation; Apoptosis
                                                                                                                                                                                                                               9915;
                                                                                                                                                                                                                                                            Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.4%;
42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last
                                    the
Burny A., Willems L.;
he bovine P53 tumor-suppressor cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LION; APOPTOSIS.
TRANSCRIPTION ACTIVATION (ACIDIC)
BY SINILARITY.
OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 744; DB 1
Pred. No. 7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEES
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                761A718FDC93DA59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ES -> MQEP (IN REF. -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                          Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119;
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                                                                                                                                                                                                                                                                                      Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QHT--IETYRQQQQQQHQ
                                                                                                                                                                                                                                                                                          Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
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                                                                                                                                                                                              Matches
                                                                                                                           Query Match
Best Local
                                                                                                                                                            MOD_RES
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                EMBL; U74450, ....
PIR; S51648; S51648.
HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                    ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1. Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komori H., Ishiguro N., Horiuchi M., Shinagawa "Predominant p53 mutations in enzootic bovine "Pt. Immunol. Immunopathol. 52:53-63(1996).
                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                      DNA_BIND
                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                             Nuclear
                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96401400; PubMed=880777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 13-386 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Binds DNA as SUBCELLULAR LOCATION: DISEASE: p53 is found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of transformed cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression
                                                                                                                                                                                                                                                                                                                                                                               X81704; CAA57348.1; -. D49825; BAA08629.1; -. IT74486; AAB51214.1; -.
                                                                                                                 164;
                                             53
                                                                    7
                                                                                           σ
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                         PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5:261-264(1995).
TELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNE
                                                                                         ENNAQTQFSEPQYTNLGLL----NSMDQQTQNGSSSTSPYN----TDHAQNSVTAP---
                      EPSAPAAPPPAT----PAPATSWPLSSFVPSQKTYPGNYGFRLGFLQSGTAKSVTCTYS
                                                                    ELNVEPPLSQETFSDLWNLLPENNLLSSELSAPVDDLLPYTDVATWLDECPNE--APQMP
                                                                                                                                                          380
386
                                             -SPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYS
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p53 is found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binds DNA as a homotetramer (By similarity).
                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Holstein;
                                                                                                                                                                                                                                                                             Phosphorylation; Apoptosis
                                                                                                                                                                                                         285
349
380
316
                                                                                                                                                                          385
380
                                                                                                                                                               43255
                                                                                                                                                                                                                                                                                                                                                                                                                                                             institutions as long as
                                                                                                                            30.4%;
                                                                                                                                                               WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in increased amounts in a wide variety p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear
                                                                                                                 65;
                                                                                                                                                                                                                                                                                       Transcription regulation; Activator;
                                                                                                                                                                        ₽ '>
                                                                                                                             Pred.
                                                                                                                                                                                             PHOSPHORYLATION
SIMILARITY).
                                                                                                                            Score 744; DB 1;
Pred. No. 7.1e-44;
                                                                                                                                                                                                                                          TRANSCRIPTION ACTIVATION BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                          PHOSPHORYLATION (BY SIMILARITY).
R -> T (IN REF. 2).
                                                                                                                                                                                                                     BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                                                                                                               222473F28C548F31 CRC64;
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinagawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions ng as its content is in
                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukemic cell lines.";
                                                                                                                                      Length 386
                                                                                                                                                                                                           PRPK)
                                                                                                                                                                                                                     DNA-BINDING)
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aida Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Уď
                                                                                                                                                                                                                                                                 (ACIDIC).
                                                                                                                                                                                                           (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on
                                                                                                                                                                                                                                                                                                                                                                                                                                                               o
  161
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                                             101
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RESULT 14
P53_MARMO
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16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, I
28-FEB-2003 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.; "Partial characterization of the woodchuck tumor suppressor, its interaction with woodchuck hepatitis virus X antigen in hepatocarcinogenesis."; Oncogene 15:327-336(1997).
InterPro; IPRO02117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                       EMBL; AJ001022; CAA04478.1; HSSP; P04637; ITUP.
                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                            modified and
                                                                                                                                                                                                                                                               use
                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P53_MARMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bc1-2
                                                                                                                                                                                                                                                                                                                                                                           in many types of cancer.
SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Binds DNA as a homotetramer (By SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: p53 is found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression
                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                           SEASE: p53 is found in increased amounts in a transformed cells. p53 is frequently mutated
                                                                                                                                                                                                                                     non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPGESRAHSSHLKSK----KRPSPSCHKKPMLKR 380
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Last sequence update)
Last annotation update)
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Sciurognathi; Sciuridae;
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                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity)
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RESULT 15
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA_BIND
                                                     Gene
                                                                                                                                                                                Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Petrebrata; Euteleos
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias
                                                                                                                                                                                                                                                           P53_ORYLA STANDARD; PRT; 352 AA.
P79820; Q9PSU7; Q9PSU8;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
             SEQUENCE FROM N. STRAIN-Himedaka;
                                                              Krause M.K., Rhodes L.D., van Beneden R.J., "Cloning of the p53 tumor suppressor gene from (Oryzias latipes) and evaluation of mutational exposed fish.";
                                                                                                                                                                                                                                                   TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-oncogene; D
Nuclear protein;
DOMAIN 1
                                                                                                                   MEDLINE=97305153; PubMed=9161419;
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                    NCBI_TaxID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
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                                                                                                                                 Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                        FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                             RQQQQQQHQHLLQKQTSIQSPSS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAPSPATSWPLSSSVPSQNTYPGYYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCP
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                                                                                                                                                                                                                                                                                                                                                                                               KGQSTSRHKKIIFKR---EGPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSPQPKKKPLDGEYFTLKIRGRARFEMFQELNEALELKDAQAEKEPGESRPHPSYLKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHT------IETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGNLLGRNSFEVRVCACPGRDRRTEEENFRKR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNT-----HGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQLWVDSTPPPGTRVRAMAIYKKSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGN
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391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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323
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 Gumerlock P.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 738.5; 1
Pred. No. 1.7e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSCRIPTION ACTIVATION (ACIDIC)
Wong J.T.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E1DE5DB84BA40182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
 Hsieh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -GPDEALQMSAAPAPKAPTPAASTL
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                                                                                           the Japanese medaka
                                                                             hotspots in MNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GEPCPEPPPRSTKRALPNGT
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 D.P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                           Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activator
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SEQUENCE
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DOMAIN
DOMAIN
DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF003949; AAD01195.1; -. EMBL; AF003950; AAD01196.1; -. HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: Acts a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation of cDNAs encoding the p53 tumor suppressor gene in the Japanese Medaka (Oryzias latipes).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00870; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                   297
                                                                   242
                                                                                   237 DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSI 296
                                                                                                                                   183 QLAQYFEDPYTKRQSVTVPYEPPQPGSEMTTILLSYMCNSSCMGGMNRRPILTILTLET-
                                                                                                                                                                        177
                                                                                                                                                                                                        128
                                                                                                                                                                                                                                        117
 288
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                                                                                                                                                                                                                                                                                                                                           al Similarity
148; Conserv
KRKKSHSSGEEEDNREVFHFEVYGRERYEFLKKINDGLELLE 329
                              KKRRS-----PDDELLYLPVRGRETYEMLLKIKESLELMQ 331
                                                               EGLVLGRRCFEVRICACPGRDRKTEEESRQKTQPK-----KRKVTPNT----SSS
                                                                                                                                                     SHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETR 236
                                                                                                                                                                                                   IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN 176
                                                                                                                                                                                                                                                                        EPVPTNEVNPPPTTVPVTTDYPGSYELELRFQKSGTAKSVTSTYSETLNKLYCQLAKTSP
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                                                                                                                                                                                                                                                                                                                                                                                                             352 AA;
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302
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48 TRANSCRIPTION ACTIVATION (ACIDIC).
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                                                                                                                                                                                                                                                                                                                                           40; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Score 737.5; DB 1
Pred. No. 1.8e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                           ISSING (IN REF. 1).
196868A66351BFF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 352;
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Search completed: August Job time: 10.1754 secs

7, 2003, 09:47:29

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Minimum DB :
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No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                        Score
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Match
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
     100.0
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sp_virus:*
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Q9ubv9 homo sapien
Q9ubv9 homo sapien
Q9plb4 homo sapien
Q9pl6 rattus norv
O75080 homo sapien
O89097 mus musculu
Q991e2 rattus norv
Q9h3d3 homo sapien
Q9plb7 homo sapien
Q9plb7 homo sapien
Q9pld7 rattus norv
Q99jd8 rattus sapien
Q9h3d4 homo sapien
                                                                                                                                         Q9up26 homo sapien
Q9p1b5 homo sapien
Q9qwy9 mus muscul
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Q96KR0	Q9CU77	Q8NHW9	Q8TDY6	Q8TDY5	Q9JJP2	Q9JJP1	Q9W664	Q8C826	Q98SW0	088897	Q99JE0	Q99JE1	Q9H3D2	О8ЛНZ6	Q8JFE3	Q8JHZ5	088899	Q99JD9	Q9UP74	075922	Q9Н3Р8	Q9NPH7	Q9P1B6	Q9DEC7	Q9JJP6	Q99JE3	868880	Q9UE10
Q96kr0 homo sapien	Q9cu77 mus musculu	omo	omo	Q8tdy5 homo sapien	Q9jjp2 mus musculu	Q9jjp1 mus musculu	Q9w664 barbus barb		Q98sw0 xenopus lae	O88897 mus musculu	Q99je0 rattus norv	Q99je1 rattus norv	Q9h3d2 homo sapien	Q8jhz6 brachydanio	Q8jfe3 brachydanio	ora	O88899 mus musculu	catt	₫	homo		homo	homo sa	Q9dec7 gallus gall	rattus	Q99je3 rattus norv	O88898 mus musculu	Q9ue10 homo sapien

ALIGNMENTS

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HSSP; InterP	EMBL; AF124537; AAG45611.1;	R EMBL; AF124536; AAG45611.1; JOINED.	EMBL; AF124534; AAG45611.1;	EMBL; AF124533; AAG45611.	EMBL; AF124532; AAG45611.1;	EMBL; AF124531; AAG45611.1;	EMBL; AF124530;	EMBL; AF124539; AAG45611.1;	R EMBL; AF075433; AAC62638.1;	-!- SIMILARITY: BELONGS TO THE P53		Submitted (JAN-1999) to the EMBL/Ge	Hagiwara	P SEQUENCE FROM N.A.		Mol. Cell 2:305-316(1998).	transactivating, death-inducing, and dominant-negative act	"p63, a p53 homolog at 3q27-29	Andrews N.C., Caput D., McKeon F.;	Yang A.	MEDLINE=98448095; Pu	P SEQUENCE FROM N.A.		NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini	Eukaryota; Me	S Homo sapiens (Human).	N P63.)E DN P63 beta.	01-OCT-2002 (TrEMBLrel. 22, Last annotation	01-MAY-2000 (TrEMBLrel.	01-MAY-2000 (TrEMBLrel.		D Q9UP26 PRELIMINARY; PRT; 461 AA.	RESULT 1 Q9UP26

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Matches 461
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Q9P1B5;
Q1-OCT-2000
Q1-OCT-2000
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 EMBL;
EMBL;
EMBL;
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EMBL;
                                                                                                             Tani M.,
Yokota J.
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PRINTS; PR00386; P53SUPPRESSR.
Probom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                            01-OCT-2000 (TYEMBLTel. 15, Created)
01-OCT-2000 (TYEMBLTel. 15, Last sequence up
01-OCT-2002 (TYEMBLTel. 22, Last annotation
P51 isoform delNbeta.
                                                                       "Mutation and expression (Neoplasia 1:71-79(1999).
-!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
                                                                                                                              SEQUENCE FROM N.A. MEDLINE=20388515;
                                                                                                                                                         NCBI_TaxID=9606;
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hes 461;
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                           AF116760;
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AF116758;
AF116759;
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AAAF43492.1;

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Primates;
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Pred. No. 4
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4.2e-199;
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EMBL; AF116766; AAF43492.1;
EMBL; AF116767; AAF43492.1;
EMBL; AAF1637; TYCS.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                Q9QWY9;
01-MAY-2000
01-MAY-2000
01-OCT-2002
MO1. Cell 2:3U5-310(12270): NUCLEAR (-!- SUBCELLULAR LOCATION: NUCLEAR (-!- SIMILARITY: BELONGS TO THE P53 EMBL; AF075438; AAC62643.1; -.
                                    Yang A., Kaghad M., Gillett E., I
Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, 6
transactivating, death-inducing,
Mol. Cell 2:305-316(1998).
                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PR0SITE; PS00348; P53; 1.
                                                                                                                                                            DN p63 beta.
TRP63.
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SEQUENCE 461 AA;
                                                                                       SEQUENCE FROM N.A. MEDLINE=98448095;
                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                     SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
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AAF43492.1;
AAF43492.1;
                                                                            PubMed=9774969;
., Gillett E., Fleming
                                                                                                                              Chordata;
Rodentia;
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Pred. No. 1
                                                                                                                              Craniata; Vertebrata; Sciurognathi; Muridae;
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                                               encodes multiple produce, and dominant-negative
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                                                                             M.D.,
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Best Local Sim
Matches 456;
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Interpro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
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Q9UBV9;
Q1-MAY-2000 (
Q1-MAY-2000 (
Q1-OCT-2002 (
DN P63 alpha.
P63.
                                                                                              SEQUENCE FROM N.A.

MEDILINE=98448095; PubMed=9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V
Rang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V
Randrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activity
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                   SEQUENCE FROM N.A.
Lee L.A., Walsh P.,
Dellavalle R.P., Taj
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                     P., Prater C.A., Targoff I.N., K
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Pred. No. 3
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                   K.M., Chorzelski T.P.,
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[3]
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-I- SIMILARITY: BELONGS T-
EMBL; AF075431; AAC62636.
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Nuclear protein.
SEQUENCE 586 AA; 65756
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Pfam; PFO0870;
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AF124530, AAG45610.1,
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AF124533, AAG45610.1,
AF124534, AAG45610.1,
AF124536, AAG45610.1,
AF124537, AAG45610.1,
AF124537, AAG45610.1,
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AF124538;
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IPR002117; I
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the EMBL/GenBank/DDBJ databases
: NUCLEAR (BY SIMILARITY).
TO THE P53 FAMILY.
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Nuclear [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSTTE; PS00348; P53; 1.
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HSSP; P04637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=20388515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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P51 isoform
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LI; AF116759; AAF43491.1; JOINED.

BL; AF116759; AAF43491.1; JOINED.

LI; AF116761; AAF43491.1; JOINED.

LI; AF116761; AAF43491.1; JOINED.

LI; AF116763; AAF43491.1; JOINED.

BL; AF116764; AAF43491.1; JOINED.

BL; AF116766; AAF43491.1; JOINED.

BL; AF116765; AAF43491.1; JOINED.

BL; AF116766; AAF43491.1; JOINED.

BL; AF116766; AAF43491.1; JOINED.

BL; AF116766; AAF43491.1; JOINED.

BL; AF116768; AAF43491.1; JOINED.

BL; AF116768; AAF43491.1; JOINED.

BL; AF116768; AAF43491.1; JOINED.

BL; AF116768; AAF43491.1; JOINED.
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OCT-2000 (TrEMBLrel. 15, Last seq
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                                                                                      SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLLQKQTSIQ
                                                                                                                                                                                         YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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                                                                                                                                                                                                                                      VMTPPPQGAVIRAMPYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                       SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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                                                                         SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQQQHQHLLQKQTSIQ
                                                                                                                         {\tt LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR}
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                                                                                                                                                                                                                                                                                                                                                                          98.8%; Score 2421; DB 4; ilarity 100.0%; Pred. No. 1.7e-196; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             AA; 65726 MW;
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K., Kawahara C.,
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FEBS Lett. 501:121-126(2001).
FEBS Lett. 501:121-126(2001).
FEBS Lett. SOI:121-126(2001).
FEBS Lett. Soi:121-126(2
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ProDom; PD002681; P53; 1
PROSITE; P500348; P53; 1
Nuclear protein.
SEQUENCE 461 AA; 5139
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01-JUN-2001
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
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MEDLINE-21363378; PubMed-11470269;
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"Identification and tissue distribution of novel KET/p63 splice
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Last sequence up
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Pred. No. 2.2e-196;
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C -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
C -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
R EMBL; AB010153; BAA32433.1; -.
R HSSP; P04637; 1YCS.
R InterPro; IPR002117; P53.
R InterPro; IPR002117; P53.
R Pfam; PF00970; P53; 1.
R Pfam; PF00970; P53; 1.
R Pfam; PF000386; P53; 1.
R PGOSITE; PR001541; P53; 1.
R SMART; SM00454; SAM; 1.
R PNOSITE; PS00348; P53; 1.
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075080;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Tanaka T., Shinkai Y., Kato H.;
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            DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
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                                                        SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIV
                                             SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Catarrhini;
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Tanaka T., Shinkai Y., Kato H.;
Tanaka 
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
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MEDLINE-98448095; Pu
Yang A., Kaghad M.,
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                                                         SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKQTSIQ
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SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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Researches 2;
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Sciurognathi; Muridae;
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Best I
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-I- SIMILARITY: BELONGS TO THE I
EMBL; AJ277447; CAC37099.1; -.
HSSP; P04637; IYCS.
InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PP00870; P53; I.
PRINTS; PR00386; P53SUPPRESSR.
PPODOM; PD002881; P53; 1.
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Q99JE2;
Q1-JUN-2001 ('
01-JUN-2001 ('
01-OCT-2002 ('
DN KET alpha )
P63.
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Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269; Bamberger C., Schmale H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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Lett. 501:121-126(2001).
Lett. 501:121-126(2001).
The p53
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                                                                   YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                                            WTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                              LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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                         SPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAG
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1 (TrEMBLrel.
2 (TrEMBLrel.
586 AA; 65732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Last annotation updat
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Pred. No. 8.6e-194;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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Query Match
Best Local
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01-MAR-2001 (TrEMBLrel. 10
01-MAR-2001 (TrEMBLrel. 11
01-OCT-2002 (TrEMBLrel. 2
TA p63 beta.
                                                                                                                                                                                                                                                                                                                    Nuclear |
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews N.C., Caput D., McKeon F.;
p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activity mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                ProDom; PD002681; P53; PROSITE; PS00348; P53;
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PRINTS; PR00386; P53SUPPRESSR.
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Mammalia; Eutheria;
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AF124529; AAG45608.1; J
AF124531; AAG45608.1; J
AF124533; AAG45608.1; J
AF124533; AAG45608.1; J
AF124534; AAG45608.1; J
AF124535; AAG45608.1; J
AF124536; AAG45608.1; J
AF124537; AAG45608.1; J
AF124537; AAG45608.1; J
AF124537; AAG45608.1; J
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                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                         TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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              PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                             PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                           TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                       PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaghad M., Wang
PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                           PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                         PQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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                                                                                                                                                                                                                                                       Conservative
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., Wang Y., Gillett E.,
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Primates;
                                                                                                                                                                                                                                                                                                                    62433 MW;
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Last sequence up
Last annotation
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Pred. No. 5.6e-193;
0; Mismatches 0;
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RESULT 11
Q9P1B7
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Matches
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O9P1B7;
O1-OCT-2000 (TrEMBLrel. 1:
O1-OCT-2002 (TrEMBLrel. 1:
O1-OCT-2002 (TrEMBLrel. 2:
P51 isoform TAp63beta.
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PROSITE;
Nuclear F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO Pfam; PF00870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutation and expression of the p51 Neoplasia 1:71-79(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tani M.,
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PD002681; P53; 1.
; PS00348; P53; 1.
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PYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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IPRO02117; P53.
0870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                   516 AA;
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K., Kawahara C.,
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99.8%;
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Pred. No. 2e-192;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 442; Conser
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Caput D., McKeon F.;
P63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.
Mol. Cell 2:305-316(1998).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR SCATION: NUCLEAR (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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Q9QWZ0;
01-MAY-2000
01-MAY-2000
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TA*p63 beta.
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Mus musculus (Mouse).

Mus myota; Metazoa; Chordata; (
""karyota; Metazoa; Rodentia;
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 555 AA; 62454 MW;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98448095; PubMed-9774969; Yang A., Kaghad M., Gillett E., Fleming M.D.,
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                                                                                         TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                       PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                              PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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Pred. No. 5e-191;
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Q99JD7;
Q1-JUN-2001
Q1-JUN-2001
Q1-OCT-2002
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-!- SIMILARITY: BELONGS TO THE EMBL; AJ277452; CAC37104.1; -.
HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Wistar; TISSUE-Tongue;
MEDLINE-21363378; PubMed-11470269;
Bamberger C., Schmale H.;
"Identification and tissue distribution of
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variants.";
FEBS Lett. 501:121-126(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           norvegicus (Rat).
PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                        LSMPSTSHCTPPPPYPTDCSIVRIWQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP
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                                                                                                                                                                                                                                                                                                                                                                              538 AA; 60326 MW;
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(TrEMBLrel. 17, Last seq
(TrEMBLrel. 22, Last ann
                                                                                                                                                                                                                                                                                                   Conservative
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98.7%;
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                                                                                                                                                                                                                                                                                                 Score 2352; DB 11;
Pred. No. 1e-190;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY)
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Matches 441
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Q99JD8;
01-JUN-2001
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01-OCT-2002
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ProDom;
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pres Lett. 501:121-126(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1. Nuclear protein. SEQUENCE 555 AA; 62426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
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HSSP; P04637; 1YCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21363378; PubMed=11470269;
Bamberger C., Schmale H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Wistar; TISSUE=Tongue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I- SUBCELLULAR LOCATION: NUCLEAR I- SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification and tissue
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                                                                                                                                                                                                                                                                                                                  TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                              PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                     PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                      PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                           PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 2352; D; Pred. No. 1.1e
3; Mismatches
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAR (BY SIMILARITY)
P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65D8854E2387C74C CRC64;
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; Murinae; Rat
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EMBL; AND16073; BAA32593 1; --
EMBL; AF116769; AAF43487 1; JC
EMBL; AF116756; AAF43487 1; JC
EMBL; AF116757; AAF43487 1; JC
EMBL; AF116757; AAF43487 1; JC
EMBL; AF116760; AAF43487 1; JC
EMBL; AF116761; AAF43487 1; JC
EMBL; AF116763; AAF43487 1; JC
EMBL; AF116764; AAF43487 1; JC
EMBL; AF116766; AAF43487 1; JC
EMBL; AF116767; AAF43487 1; JC

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O75195;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
P51 isoform TAP63ALPHA (P51B protein).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LÓCATIÓN: NUCLEAR
-i- SIMILARITY: BELONGS TO THE E33
EMBL; AB016073; BAA32593.1; -.
EMBL; AF116769; AAF43487.1; -.
EMBL; AF116756; AAF43487.1; JOINED
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TISSUE=Skeletal muscle;
MEDLINE=98324755; PubMed=9662378;
                                                                                                     PROSITE; PS00348; P53; 1.
Nuclear protein.
SEQUENCE 641 AA; 72019
                                                                                                                                                                                                PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                     InterPro; IPR002117; P53.
InterPro; IPR001660; SAM.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osada M., Ohba M., Kawahara C., Ishioka C., Kar
Ikawa Y., Nimura Y., Nakagawara A., Obinata M.,
"Cloning and functional analysis of human p51,
functionally resembles p53.";
Nat. Med. 4:839-844(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neoplasia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P04637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutation and expression of the p51 gene leoplasia 1:71-79(1999).
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Search completed: August Job time : 39.092 secs 7, 2003, 09:51:43

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Human p53 homologu	lung canc	oncogene p6	O	Human p63 protein	cell regu	р5	gene p5	tumo	lung	_	lung	5	lung		p53 h	lung	p63	p40 p	cell	cell regula	oncogene	Human oncogene p51	cell regu	p53	lung can	oncogene	oncogene p5	p63 protein	oncog	cell	e cell regula	cance		lung cancer	Human oncogene p63

ALIGNMENTS

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RESULT 1
AAY05957
ID AAY0
XX
Cell regulatory protein; p63; hu-deltaNp63 beta; human; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
         N-PSDB; AAX58576
                 WPI; 1999-277595/23
                                   McKeon F,
                                                                                                                                                                                                                                                           AAY05957;
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                                                                          29-MAY-1998;
15-OCT-1997;
                                                                                                      02-OCT-1998;
                                                                                                                        22-APR-1999
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                                                                                                                                                            Homo sapiens.
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                                  Yang A;
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97US-0062076.
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                       CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP 393
                                                                                                            SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
                                                                                                                                                                           LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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                                                                                    SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
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RESULT 2
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ABG95133

standard; Protein;

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TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120

TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK

DP GA

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MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS

60

Query Match Best Local

Similarity

100.0%;

Score 2082; DB 23; Pred. No. 1.4e-182; ; Mismatches 0;

Conservative

0;

Indels

0;

Gaps

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cell population, treating proliferative diseases associated with mutant correction (HSP)-90, or selectively treating cells expressing (II) correction genetically-defined disease with chromosomal aberration yielding concogenic fusion protein, treating cancerous cells containing fusion concogenic fusion protein, treating cancerous cells containing fusion protein in heterogenous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. CC cellular protein isoform dependent on heat shock protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoletic disorder such as T or B cell (lymphoma, chronic myeloid leukaemia (CMI), ALL, AML, NHL and CMMI, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and contain and contain the method is also useful for treating viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSP-90; rheumatoid arthritis; cancer; haematopoletic disorder; rell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NIL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosome aberration; oncogenic fusion protein; proliferative disease; cellular protein isoform;
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Sequence
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393 AA;
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                                          amino acid sequence of a human
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                                                                                                                                                                                Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
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           protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically defined disease with chromosomal aberration yielding
                                                                    The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant
  oncogenic
                                                                                                                                             Disclosure;
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DB; ABS73331.
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  protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinoma; Ewing's sarcoma; melanoma; liposarcoma
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treating cancerous
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                                                                                                                                 Key
                                                                                                                                                                                                                            Human p51 protein
                                                                                                                                                                                                                                                     07-JAN-2000
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353..397
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07-0CT-1999

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RESULT 5
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AC AAY0
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AC Huma
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DT 16-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 379;
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 Cell regulatory protein; p63;
                           Human cell regulatory protein p63, isoform huTAp63 gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human p51 protein, which is related to p53 and has cell proliferation regulation and tumour suppression activity. The p51 gene can be used in the investigation, diagnosis and treatment of diseases such as cancer, with which the p53 family cell proliferation regulation is associated. The p51 protein may be used for screening potential agonists and antagonists of its regulatory function,
                                                         16-AUG-1999
                                                                                    AAY05955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 147-148; 163pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New p53 related human gene p51, useful for diagnosis, treatment of cancers and screening for potential cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAKA ) OTSUKA PHARM CO LTD (IKAW/) IKAWA Y.
                                                                                                              AAY05955 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                               430 KQSDVFFRHSKPPNRSVYP 448
                                                                                                                                                                                               375 KQSDVFFRHSKPPNRSVYP 393
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                                                                                                                                                                                                                                                                                                                                                                                                       190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPSSTFDALSPSPAIPSN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                      ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                                                                                                                                                                                                                    ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                                                                                                                                                                                                                                                           GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                        GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                               PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                    PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                PYYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drugs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 AA;
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                                                      (first entry)
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                                                                                                            Protein; 448
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100.0%; Pr
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huTAp63 gamma; TAp63 gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 448;
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differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents human p63 isotype TAp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. DeltaN isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a DCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 13g27-29. At least 6 different isotypes exist. Splice variants
                                                        cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAN5953-64), polynucleotides (see AAN5953-64) and anti-p63 anti-p63 antiodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Fig 11; 161pp; English.
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N-PSDB; AAX58574.
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cell proliferation; cell differentiation; therapy.
                                         transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated p63 cell regulatory protein for, e.g. treatment of
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15-OCT-1997;
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97US-0062076.
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Sequence 448 AA;

Length

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Best Local Similarity
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                                                                                                                             70
                PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
                                                                                                                                             PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPSSTFDALSPSPAIPSN
                                                                TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                           PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
PYYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
                                                                                                                                                                                           Conservative
                                                                                                                                                                                   96.6%; Pro
100.0%; Pro
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                                                                                                                                                                                                        Score 2011; DB 20;
Pred. No. 5.6e-176;
                                                                                                                                                                                           Mismatches
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Indels

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Gaps

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249

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  Query Match
Best Local Similarity
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
                                                                                                                                                                                          This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-cells isolated from a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                            Sequence
                                                                                                                        are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 247-249; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung in a patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-2000; 2000WO-US08896
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ine; detection.
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DB; AAC66029.
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99US-0466396.
99US-0476496.
2000US-0480884.
2000US-0510376.
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  96.6%;
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  Score 2011; DB 21;
Pred. No. 5.6e-176;
                         Length
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RRESULT 7
AAB82128
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                                                                                            Chimera gene of the p53 family, useful for gene of cancer, comprises a transcription activating
                                                                                                                                                                                                                                             (IKAW/)
(SAKA )
                       Example 1; Page
                                                                     binding
                                                                                                                                                                      WPI; 2001-268293/28
N-PSDB; AAF86588.
                                                                                                                                                                                                                                                                                                                     09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                                                                                                   09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2000.
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OTSUKA PHARM
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                         30-32;
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1..59
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                 57pp; Japanese
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RESULT 8
ABG95127
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DT 04-D
XX Chro
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KW Troe
KW acut
KW papi
KW papi
KW papi
KW rhab
OS Homo
XX Homo
XX Homo
XX 12-S
XX 01-M
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                                                                                                                                                                                                                           Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 9 HSP-90; rheumatoid arthritis; cancer; haematopoiettic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute myeloid leukaemia; ALL; ALL; APL; HNL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a chimera gene of p53 family encoding a transcription activating region, a DNA binding region, and an oligomer formation region of different p53 family proteins. The chimeric gene can be used for gene therapy of p53 variant human tumours, and analysis of the function of the p53 family gene. The present sequence was used in the
                                                 01-MAR-2001; 2001US-272751P.
                                                                               01-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2002
                (CONF-)
                                                                                                                 12-SEP-2002
                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                              rhabdomyosarcoma; synovial sarcoma; viral infection.
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                CONFORMA THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Pred. No. 5.6e-176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oncogenic fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. p53), or selectively treating cells expressing mutant protein or cellular protein isoform in a patient heterozygous for (II). The method is useful for treating a disease e.g. haematopoletic disorder such as T or B cell. lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) involving administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding treating genetically-defined disease with chromosomal aberration yielding
                                      ABG95137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                        standard;
                                                                                                                                                                                                                        ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQXHLLSACFRNELVEPRRETP
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           describes a method of treating genetically-defined disease th chromosomal aberrations yielding oncogenic fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating cancerous cells containing (I) in a heterogeneous
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                                      Protein;
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Pred. No. 5.6e-176;
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04-DEC-2002 (first entry)

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CC protein or cellular protein isoforms (II) dependent on heat shock protein (HSP)-90, or selectively treating cells expressing (II) CC involving administering HSP90-inhibitor. The method is useful for CC involving genetically-defined disease with chromosomal aberration yielding CC oncogenic fusion protein, treating cancerous cells containing fusion CC protein in heterogeneous cell population, treating proliferative disease CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g. CC protein isoform in a patient heterozygous for (II). The method is useful CC protein isoform in a patient heterozygous for (II). The method is useful CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML, CC or a disease characterised by a solid tumour such as papillary thyroid CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rabbdomyosarcoma and CC synovial sarcoma. The method is also useful for treating viral CC infections. This is the amino acid sequence of a human oncogenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                    PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
                                                               TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
PYYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV
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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein (BSP)-90, or selectively treating cells expressing (II) involving administering (HSP90-inhibitor. The method is useful for

treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion

protein in heterogeneous cell population,

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                                                                                                                                                              Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90
                                                                                                                                                                                                                           WPI; 2002-698710/75.
                                                                                                                             Disclosure; Page 354-356; 389pp; English
                                                                                                                                                                                                                                                                                               01-MAR-2001; 2001US-272751P
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                                                                                                                                                                                                                                                                                                                                                                                                                  chabdomyosarcoma;
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  Wang T,
                                                                                                                                 12-DEC-2000;
07-MAY-2001;
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                                                     CORIXA CORP
Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQSDVFFRHSKPPNRSVYP 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer associated protein sequence SEQ ID NO:340
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                                                                                                   2001US-0850716.
2001US-0897778.
                                                                                                                                                                                                                                                                                                                                                                                                                      cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
  P
  Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                    lung
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                                                                                                                                                                                                                                                                                                                                                                                                                 tumour; cytostatic; gene therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448
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Pred. No. 5.6e-176;
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  Kalos
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RESULT 12
ABB74991
ID ABB74
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AC ABB74
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DT Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92466 and ABP61866 to ABP61992 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes isolated human lung carcinoma polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide detecting in the sample, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel lung carcinoma polynucleotide sequences and polypeptides oby the polynucleotides, useful in pharmaceutical compositions surfaceines and as markers to indicate the presence of lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McNeill PD, Fanger
Carter D, Watanabe
                                                                                          ABB74991 standard; Protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local 379;
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                                                                                                                                                                                                                                                                                             GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                      PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 329-330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Peckham DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381pp;
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                                                                                                                                                                                                  393
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Pred. No. 5.6e-176;
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Foy TM;
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01-MAY-2002

(first entry)

Human p53 homologue isoform,

p63 (L530S)

protein

SEQ

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12-DEC-2000;
07-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                  The present invention describes human lung tumour proteins. Human lung tumour proteins and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, tusion proteins, Teell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL4930 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang T,
McNeill
Vedvick
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotides encoding lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 322-323; 374pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2000;
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DB; ABL49248.
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                                                                                                    PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                   TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
           ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                        GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                        PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                            PQYTNLGLLNSMDQQTQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN
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                                            GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
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2000US-0630940.
2000US-0643597.
2000US-0662786.
2000US-0685696.
2000US-0735705.
2001US-0850716.
                                                                                                                                                                                                                                                                          Conservative
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Fanger N, Retter MW,
Carter D, Watanabe Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                              96.6%;
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                                                                                                                                                                                                                                                                                Score 2011; DB 23;
Pred. No. 5.6e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor polypeptides, useful for treating
immune response -
                                                                                                                                                                                                                                                                         Mismatches
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Marnerakis M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peckham DW;
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                                                                                                                                                                                                                                                                                               448;
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RESULT 13
ABU5641B
ID ABU56
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AC ABU56
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DT 02-A
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Lung
XW Lung
XW Lung
XW Lung
XW Int
XX
W Sma
KW Sma
KW Sma
XW Int
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PF 16
PR 11
PR 
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                                                                          The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits cancer-associated polynucleotides and polypeptides. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2001;
10-MAY-2001;
09-NOV-2001;
13-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a lung cancer-associated transcript in a cell from a patier for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                       polypeptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EOSB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003-093161/08.
DB; ABX76134.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer-associated polypeptide #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Page 196; 453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EOS
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2001US-339245P.
2001US-350666P.
2001US-334370P.
2002US-372246P.
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                                                             invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n a patient from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atelectasis;
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Best Local
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The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of protein which demonstrate certain sequence identity to known tumour
                                              Claim 23;
                                                                                                                                                                                                                                                                                                         cancer; tumour suppressor; cell cycle control; apoptosis;
cell proliferation; cell differentiation; therapy.
                                                                                                                                                                                                                                                                                                                               Cell regulatory protein; p63; mu-deltaNp63 gamma;
                                                                                                                                                                                                                                                                                                                                                                                                    AAY05964;
                                                                                                                WPI; 1999-277595/23.
                                                                                                                                      McKeon F,
                                                                                                                                                            (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                   02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                     Mouse cell regulatory protein
                                                                                                                                                                                                                                                                                                                                                                             16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY05964 standard; Protein;
                                                                            New isolated p63 cell regulatory protein
                                                                                                                                                                                   29-MAY-1998;
15-OCT-1997;
                                                                                                                                                                                                                                         22-APR-1999.
                                                                                                                                                                                                                                                                WO9919357-A2
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                                                                                                      AAX58583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KQSDVFFRHSKPPNRSVYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTEDALSPSPAIPSN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQSDVFFRHSKPPNRSVYP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM
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                                            20; 161pp;
                                                                                                                                                                                 98US-0087216.
97US-0062076.
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100.0%;
                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                         389
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Pred. No. 5.6e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448
                                                                                                                                                                                                                                                                                                                                                      p63, isoform deltaNp63 gamma,
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                                                                               treatment
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          proteins
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RESULT 15
AAYO5961
ID AAYO5
XX AAYO5
XX AAYO5
XX I6-AU
DT 16-AU
XX Mouse
XX Cell
KW Cance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identified by screening a CDNA library with a probe corresponding to exons 5-9 of p63 At least 6 different isotypes exist. Splice variants differing at the C-terminus are designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltan beta and gamma forms, while p63 members differing in the N-terminus are designated as deltan and TA forms, where the deltan form lacks the transactivation domain. The present sequence represents mouse p63 tsotype mu-deltany63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous of ifferentiation, both benign and neoplastic. Deltan isotopes of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
Cell regulatory protein; p63; muTAp63 gamma; TAp63 gamma; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suppressor proteins p53 and p73. Mouse p63 cDNA was isol RACE. Sequencing of the amplification product indicated amplified cDNA possessed a truncated N-terminus, i.e. the transactivation domain was absent. Additional splice variances
                                                                                                                      16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                           Mouse cell regulatory protein p63, isoform muTAp63 gamma
                                                                                                                                                                                                  AAY05961 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic animals.
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                                                                                                                                                                                                                                                                                                                   CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLILVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                   CFRNELVEPRGEAPTQSDVFFRHSNPPNHSVYP
                                                                                                                                                                                                                                                                                                                                                                               SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGRRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDA----FRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 AA;
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                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection and diagnosis, and in the production
                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.5%;
97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2009; DB 2
Pred. No. 7e-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse p63 cDNA was isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Additional splice variants were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lated using that the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Fig 17; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using RACE. Sequencing of the amplification product indicated that the amplified cDNA possessed a truncated N-terminus, i.e. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: FILE REFERENCE: 201121.455CB
CURRENT APPLICATION AND DIAGNOSIS OF LUNG CA
FILE REFERENCE: 210121.455CB
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
CORTWANDE: FASTERD for Mindows Version 3 0
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US-09-606-421B-340
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; ORGANISM: Homo sapiens
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  Sequence 340, Application Patent No. 6531315
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Best Local Similarity
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APPLICANT: Wang, To
APPLICANT: Fan, Liq;
APPLICANT: Kalos, M.
APPLICANT: Bangur, C.
APPLICANT: Hosken, b.
APPLICANT: Fanger, C.
APPLICANT: Li, Samue
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Henderson, Robert A.
McNeill, Patricia D.
JENTION: COMPOSITIONS
                                 Wang, Aljun
Skeiky, Yasir A.W.
                                                                                                                      Wang, Tong
Fan, Liqun
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 340
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                   Sequence 343, Application US/09643597 Patent No. 6426072
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Bangur, Chaitanya (Hosken, Nancy Fanger, Gary R. Li, Samuel X.
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Pred. No. 1.3e-184;
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AND

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APPLICANT: Wang, TUNYAU,
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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                                                                                                                             FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/OS
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Vo
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CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 343
LENGTH: 461
                 Query Match
Best Local Similarity
   Matches
                                                                  ORGANISM: Homo
09-542-615A-343
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                                                                                                TYPE: PRT
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APPLICANT: L1, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C9

CURRENT APPLICATION UNUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 343

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Best Local S
Matches 361
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APPLICANT: Fan, L
APPLICANT: Kalos,
APPLICANT: Bangur
APPLICANT: Hosker
APPLICANT: Fanger
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                                                                                                                                                                                                                                                                                                                                 LENGTH: 461
TYPE: PRT
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YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                               VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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Fanger, Gary R.
Li, Samuel X.
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Bangur, Chaitanya
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Pred. No. 2e-172;
3; Mismatches 7;
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHOI
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG (
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION UNGMER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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US-09-643-597-341
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SEQ ID NO 341
LENGTH: 356
TYPE: PRT
ORGANISM: Homo saplens
5-09-643-597-341
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Best Local :
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APPLICANT:
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APPLICANT:
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             SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQK 355
                                                                       LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                              YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                      VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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Fanger, Gary R.
Li, Samuel X.
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                                                       LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPSRQNTHGIQMTSIKKRR
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Fan, Liqun
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99.7%;
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Pred. No. 5.9e-171;
0; Mismatches 1;
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LUNG CANCER
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; SEQ ID NO 2
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-277-196-2
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Compounds and Methods for ITTLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE REFERENCE: 210121.455C8
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 341
LENGTH: 356
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US-09-277-196-2
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APPLICANT: Trink, Barry
APPLICANT: Jen, Jin
APPLICANT: Ratovitski, Edward
APPLICANT: Sidransky, David
TITLE OF INVENTION: p40 Protein Acts as an Oncogene
FILE REFERENCE: 01107.79765
                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                Sequence 341, Application Patent No. 6518256
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Patent No. 6476206
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Best Local
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CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/079736
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 5.9e-171;
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APPLICANT: Skelky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C9

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 341

LENGTH: 356

TYPE: PRT
ORGANISM: Homo sapiens

US-09-606-421B-341
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US-09-606-421B-341
; Sequence 341, Application US/09606421B
; Patent No. 6531315
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Best Local Similarity
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Local Similarity 99.7%;
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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
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Pred. No. 5.9e-171;
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Pred. No. 5.9e-171;
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CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 338
ELENCTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
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              SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSA 360
                                                                  LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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Henderson, Robert A.
McNeill, Patricia D.
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                                                    LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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Fan, Liqun
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Li, Samuel X.
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APPLICANT: Wang, Touyoon,
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOF
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAI
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; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-542-615A-338
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US-09-542-615A-338
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                                                                                                              Sequence 338, Application US/09606421B Patent No. 6531315
                                                                                               GENERAL
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    APPLICANT:
                                APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun APPLICANT: Kalos, Michael APPLICANT: Bangur, Chaitz
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                                                                                               INFORMATION:
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Hosken, Nancy
Fanger, Gary R.
                                Bangur, Chaitanya
                                               Kalos, Michael D.
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Pred. No. 1.2e-170;
4; Mismatches 9;
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APPLICANT: Li, Samuel ...

APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
                                                                 APPLICANT: Wang, Alju.,
APPLICANT: Skeiky, Yasir A.W.,
APPLICANT: Skeiky, Yasir A.W.,
APPLICANT: Henderson, Robert A.,
APPLICANT: McNeill, Patricia D.,
TITLE OF INVENTION: COMPOSITIONS AND ME',
TITLE OF INVENTION: AND DIAGNOSIS OF LU
TOPPERENCE: 210121.455C11
                                                                                                                                                                                                                                                                                                                                                                                              US-09-643-597-152
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Best Local Similarity
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
SEQ ID NO 152
                                                     CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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                    FastSEQ for Windows Version
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                                                                                                          LUNG
                                                                                                                            METHODS FOR
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RESULT 15
US-09-480-884A-152
; Sequence 152, Application US/09480884A
"arent No. 6482597
                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-480-884A-152
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Best Local S
Matches 357
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CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
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TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                       MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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92.2%;
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                                                                                                              Score 1860; DB 4;
Pred. No. 5.9e-170;
5; Mismatches 9;
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Pred. No. 5.9e-170;
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                                                                      VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                             SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA 360
                CFRNELVEPRRETPKQSDVFFRHSKPP 387
                                   SPDDELVYLPVRGRETYEMLVKIKESLELMQYLLQHTIETYRQQQQQQQHQHLLQK----
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QTSIQSPSSYGNSSPP 371
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Search completed: August 7, 2003, 09:54:56 Job time: 11.8414 secs (OTAZU) XNAJA 32A9 ZIHT

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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                                                                                                                                                                                                                                                  Score
         2011
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1    /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2    /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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Copyright (c) 1993 - 2003 Compus
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                       DВ
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15
                   0 US-09-735-705-341

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10 US-09-897-778-341

10 US-10-274-874-2

0 US-09-735-705-338

10 US-09-735-705-338

10 US-09-735-705-152
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US-09-897-778-340
US-09-735-705-343
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2781.719 Million cell updates/sec
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Sequence 340, App
Sequence 340, App
Sequence 343, App
Sequence 343, App
Sequence 341, App
Sequence 341, App
Sequence 341, App
Sequence 341, App
Sequence 2, Appl1
Sequence 338, App
Sequence 338, App
Sequence 338, App
Sequence 152, App
Sequence 152, App
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45	44	43	42	41	40	39	38	37	36	35	34							27	26	25	24	23	22	21	20	19	18	17	16	
679.5	692	694	696	699	700.5	703	707	707	707	707	707	707	707	707	1248.5	1248.5	1248.5	1807	1813	1813	1813	1813	1813	1813	1813	1813	1813	1860	1860	
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374	381	394	390	390	353	401	428	393	393	393	393	393	393	393	636	635	420	426	680	680	680	641	641	641	516	516	516	586	586	
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	-09-968-851-	-059-	-10-		-10-146-473-	'n	-10-076-691-	-10-160-290-	-10-274-		US-09-029-327-4	US-09-860-211-9	US-09-732-384-3	09-776-695-3	-09-732	US-10-155-059-3	US-10-274-874-20	US-10-274-874-19	US-09-897-778-342	US-09-850-716A-342	US-09-735-705-342	US-09-897-778-339	US-09-850-716A-339	US-09-735-705-339	US-09-897-778-344	US-09-850-716A-344	US-09-735-705-344	US-09-466-396A-152	US-09-897-778-152	
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ALIGNMENTS

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SEQ ID NO 340
: LENGTH: 448
: TYPE: PRT
: ORGANISM: Homo sapiens
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US-09-735-705-340
                                                   Query Match
Best Local S
Matches 379
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                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
                                                                                                                                                                                                                                                                     APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
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APPLICANT:
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                                                                    Local Similarity
15 PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
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ilarity 100.0%;
Conservative
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                                                  Score 2011; DB 9; ; Pred. No. 3.4e-178; 0; Mismatches 0;
                                                                                    Length 448;
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PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129

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; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-340
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US-09-850-716A-340
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 340
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
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                                                                                                                                                                                           PYYKKAEHYTEVYKRCPNHELSREFNEGQIAPPSHLIRYEGNSHAQYYEDPITGRQSYLV 194
                  ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACERNELVEPRRETP
                                                              GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
                                                                                                                            PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                           PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQSDVFFRHSKPPNRSVYP 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR 314
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     ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
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                                              RESULT 4
US-09-735-705-343
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; Patent No. US20020052329A1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-340
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US-09-897-778-340
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 340
LENGTH: 448
Type: nom
GENERAL INFORMATION:
APPLICANT: Wang, T
APPLICANT: Fan, L1
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APPLICANT: Warnerakis, Mar
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas
APPLICANT: Vedvick, Darrick
APPLICANT: Watanabe, Yoshi
APPLICANT: Henderson, Robe
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Best Local Similarity
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APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
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Vedvick, Thomas
-ter, Darrick
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 Wang, Tong
Fan, Liqun
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100.0%;
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Pred. No. 3
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Length 448; Indels

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THITITE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121, 455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 343

LENGTH: 461

TYPE: PRT

ORGANISM: Homo Sapiens
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Best Local S
Matches 361
                                                                                                                                                                                        Sequence 343, Application US/09850716A Patent No. US20020115139A1 GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
                                                                                             APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LONG CANCER
FILE REFERENCE: 210121.455C15
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Henderson, Robert A.
McNeill, Patricia D.
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Li, Samuel X.
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Pred. No. 2.2e-166;
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 343
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                                                                                                                                           Query Match
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CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
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APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
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APPLICANT: Fanger, Neil
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TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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93.3%;
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Pred. No. 2.2e-166;
3; Mismatches 7;
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SEQ ID NO 341
LENGTH: 356
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Best Local
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ORGANISM: Homo sapiens
-09-735-705-341
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
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181 YVEDDITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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                            YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
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Skeiky, Yasir A.W.
Henderson, Robert A.
McNeill, Patricia D.
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Hosken, Nancy
Fanger, Gary R.
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Pred. No. 5.7e-165;
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: Sequence 341, Application US/09897778

; Patent No. US20020147143A1
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                                                                                                         GENERAL INFORMATION:
                                       APPLICANT:
            APPLICANT:
                                                                  APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, M
APPLICANT: Fanger, Gary
APPLICANT
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Watanabe, Yoshihiro Marnerakis, Margarita Fanger, Gary R. Vedvick, Thomas S. Carter, Darrick

Peckham, David Henderson,

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; Sequence 341, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: MCN0411, Patricia D.
APPLICANT: MCN0411, Patricia D.
APPLICANT: MCN0411, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT APPLICATION SAME PROPERTY OF THE THE
CURRENT APPLICATION NUMBER: US/09/850,716A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Homo sapiens US-09-850-716A-341
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 341
LENGTH: 356
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Best Local
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                                                                                                      LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
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SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQK
                                                                                LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPSRQNTHGIQMTSIKKRR
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Pred. No. 5.7e-165;
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US-10-274-874-2
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TITLE OF INVENTION: p40 Protein Acts as an On-
FILE REFERENCE: 01107.79765
CURRENT APPLICATION NUMBER: US/10/274,874
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: US/09/277,196
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEO ID NOS: 20
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; ORGANISM: Homo sapiens
US-10-274-874-2
                                   Query Match
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Matches 354
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TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 341
LENGTH: 356
TYPE: DEST
                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 356
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Best Local Similarity
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APPLICANT: Jen, Jin
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354; Conservative
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Pred. No. 5.7e
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Pred. No. 5.7e-165;
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US-09-735-705-338
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CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
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APPLICANT:
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APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
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                                                                                                                 VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQK 355
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Fan, Liqun
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Skeiky, Yasir A.W.
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Fanger, Gary R.
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92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1867; DB 9; pred. No. 1.2e-164;
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GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: KCNeill, Patricia D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455015
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF 5EQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 338
LENGTH: 566
TYPE: PRT
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                                              RESULT 13
US-09-897-778-338
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    GENERAL INFORMATION:
                Sequence 338, Application US/09897778 Patent No. US20020147143A1
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Pred. No. 1.2e-164;
4; Mismatches 9;
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                                                          APPLICANT:
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CURRENT APPLICATION NUMBER: US/0:
CURRENT FILING DATE: 2001-06-28
RUMBER OF SEQ ID NOS: 467
                                                                                                                                                                      APPLICANT:
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APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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TYPE: PRT
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 !: Fanger, Neil
INVENTION: COM
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                                                                                       Hosken, Nancy Fanger, Gary R. Li, Samuel X.
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Fan, Liqun
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                      Skeiky, Yasir A.W.
Henderson, Robert A.
McNeill, Patricia D.
                                                                        Wang, Aijun
                                                                                                                                      Bangur, Chaitanya
                                                                                                                                                    Kalos, Michael D.
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Henderson, Robert A.
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Vedvick, Thom
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 COMPOSITIONS
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Pred. No. 1.2e-164;
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THERAPY

Indels Length 586;

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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
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US-09-850-716A-152
; Sequence 152, Application US/09850716A
; Patent No. US20020115139A1
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CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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al Similarity 92.2%;
357; Conservative
                                                               al Similarity
357; Conserva
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              MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSYTAPSPYAQPSS
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MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                               Conservative
                                                                          89.3%;
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Pred. No. 5.3e-164;
5; Mismatches 9;
                                                               5.
                                                           Score 1860; DB 10;
Pred. No. 5.3e-164;
5; Mismatches 9;
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                                               SPDDELVYLPVRGRETYEMLVKIKESLELMQYLLQHTIETYRQQQQQQQQQHQHLLQK-----
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                       CFRNELVEPRRETPKQSDVFFRHSKPP 387
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-QTSIQSPSSYGNSSPP
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Description	ID	Length DB	1 37 10	Score	Result No.
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PKQSDVFFRHSKPPNRSVYP 393	:	US-09-538-106-18 2082 1 MLYLENNAQTQFSEPQYTNL		Title: Perfect score: Sequence:	Title: Perfect : Sequence
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	ng sw model	protein search, using	rotein	1	OM protein
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probable membrane	hypothetical prote	LTR gag/pol polypr	mycelial surface a	hypothetical prote	hypothetical prote	transcription fact	protein-tyrosine-p	protein-tyrosine-p	SNF2 protein - yea	protein-tyrosine-p	transcription fact	polyketide synthas	Bassoon protein -	hypothetical prote	cellular tumor ant	cellular tumor ant	tumor suppressor p	tumor suppressor p	tumor	tumor		tumor	•	tumor		cellular tumor ant	cellular tumor ant		Description
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360 DKYRQK 365	339 ETYRQQ 344 : -	284 FRQ-NTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI 338 ::	227 ILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRP 283 : :: : : : : : : : :::: :::: ::::	167 PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRP 226 : : :	107 LYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREENEGQIAP 166 : : : :	49 VTAPSPYAQPS-STFDALS-PSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKK 106 	Query Match 40.3%; Score 839.5; DB 1; Length 396; Best Local Similarity 55.2%; Pred. No. 2.6e-58; Matches 169; Conservative 47; Mismatches 79; Indels 11; Gaps 6;	PESULT 1 THO631 cellular tumor antigen p53 - rainbow trout C;Species: Oncorhynchus mykiss (rainbow trout) C;Coessio: JH0631 R;Collidar trout p53: CDNA cloning and biochemical characterization. A;Title: Rainbow trout p53: CDNA cloning and biochemical characterization. A;Reference number: JH0631; MUID:92210006; PMID:1339362 A;Reference number: JH0631; MUID:92210006; PMID:1339362 A;Residues: 1-396 <def> A;Residues: 1-396 <def> A;Eross-references: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829 A;Eross-references: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829 A;Experimental source: liver C;Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive (Superfamily: cellular tumor antigen p53 C;Reywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho F;164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) *status predicted F;395/Binding site: phosphoryl-RNA (Ser) (covalent) *status predicted</def></def>

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A; Gene:
C; Superf
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F; 362/Bi
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(;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29376; S61531; S72313; I51639
R;Soussi, T.; de Fromentel, C.C.; Mechali, M.; May, P.; Kress, M.
oncogene 1, 71-78, 1987
                                          R;Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P. Nucleic Acids Res. 16, 11383, 1988 A;Title: Nucleotide sequence of a cDNA encoding the chicken A;Reference number: S02193; MUID:89083584; PMID:3060861 A;Accession: S02193
                                                                                                                           N;Alternate names: nuclear oncoprotein p53
C;Speciles: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S02193
R;Soussi, T; Begue, A.; Kress, M.; Stehelin, D.; May, P.
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A;Title: Overexpression of wild-type p53 interferes with A;Reference number: I51639; MUID:94134403; PMID:8302570 A;Accession: S6151
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                       A; Molecule type:
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Cellular tumor antigen p53 - chicken
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A;Residues: 1-51,'S',53-70,72-293,295-363 <HOW>
A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1;
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A;Residues: 1-23,295-363 <HOE>
A;Residues: 1-23,295-363 <HOE>
A;Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
R;Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knochel, W.
submitted to the EMBL Data Library, March 1994
      A; Residues:
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A; Accession: S72313
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Best Local Similarity
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Keywords: apoptosis; cell division control; DNA binding; homotetramer; nu
150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
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                                                                                                                                                                                                                                                                                                                                  DDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV
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                           mRNA
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54.5%;
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Pred. No. 2.9e-52;
42; Mismatches 68
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PMID:2830576
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chel, W.
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                                                                                nuclear oncoprotein.
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A;Cross-references: EMBL:x81704; NID:g602332; PIDN:CAA57348.1; PID:g602333 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; ph F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted F;385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellular tumor antigen p53 - bovine N;Alternate names: tumor-suppressor protein C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Se C;Accession: S51648 F.; Willems, L.; Burny, A.; Kett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741 C;Superfamily: cellular tumor antigen p53 C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; E;161,164,224,728/Minding site: zinc (Cys, His, Cys, Cys) #status predict F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, So
A;Description: Nucleotide sequence of
A;Reference number: S51648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-386 < DEQ>
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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MNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK
                                            G-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
                                                                                      GQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
                                                                                                                                    PSLNKLFCQLAKTCPVQLWVDSPPPPGTRVRAMAIYKKLEHMTEVVRRCPHHERSSDYSD
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Pred. No. 6.2e-51;
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A;Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID R;Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A;Title: Structure of the rat p53 tumor suppressor gene.
A;Reference number: $41149; MUID:93181268; PMID:8441680
A;Accession: $41149
A;Status: prelininary; nucleic acid sequence not shown; translating the status: prelininary; nucleic acid sequence not shown; translating the status prelininary; nucleic acid sequence not shown; translating the status prelininary; nucleic acid sequence not shown; translating the status prelininary; nucleic acid sequence not shown; translating the status of the EMBL:107909
A;Molecule type: DNA
A;Residues: 1-173,'W',175-391 < HUL>
A;Cross-references: EMBL:107909
A;Note: the nucleotide sequence was submitted to the EMBL Data Lil C;Genetics:
A;Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C;Keywords: apoptosis; cell division control; DNA binding; homote F;174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predii
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                                                                                                                                                                                                          ARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSP-DDEL
                                                                                                                                                                                                                                                                                  FRHSVVVPYEPPEVGSDYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                   TRVRAMAIYKKSQHMTEVVRRCPHHE----RCSDGDGLAPPQHLIRVEGNPYAEYLDDRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --VPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSISLNKLFCQLAKTCPVQLWVTSTPPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGSPNSMEDLFLPQDVAELLEGPEEALQVSAPAAQEPGTEAPAPVAPASATPWPLSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRQQQQQQH-QHLLQKHLLS-ACFRNELVEPRRETP 374
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                                                             LYLPVRGRETYEMLLKIKESLEL
                                                                                                                                 VRVCACPGRDRRTEEENFRKKEEHCPELPPGSAKRALPTST----SSSPQQKKKPLDGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPGESRAHSSHLKSKKRPSPSCHKKPML--KREGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RALPTNT----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALEL-----KDALDG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 6.4e-49;
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348
                                                                329
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N,Alternate names: tumor-suppressor protein p53
()Species: Mesocricetus auratus (golden hamster)
()Species: Mesocricetus auratus (golden hamster)
()Accession: JH0633
R,Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A,Title: The cDNA cloning and immunological characterization
A;Reference number: JH0633; MUID:92210007; PMID:1555773
                                                                                                                                                                 cellular tumor antigen p53 [validated] - human
N;Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppr
C;Species: Homo sapiens (man)
C;Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C;Accession: A25224; A43073; JT0436; S40773; S42689; A22837; A55080; A25397; B25397;
4905; I58354; I78850; I52681; S60153
R;Lamb, P.; Crawford, L.
                                                                                                                                                                                                                                                                                                                     RESULT 7
DNHU53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: p53
C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F;179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;395/Binding site: phosphoryi-RNA (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-396 <LEG>
A; Cross-references: GB:M75144; NID:g191414;
A; Experimental source: kidney, strain MP1
C; Genetics:
                                                                                                         Mol. Cell. Biol. 6, 1379-1385, 1986 A; Title: Characterization of the hu A; Reference number: A25224; MUID:87
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A;Cross-references: EMBL:X01405; R;Buchman, V.L.; Chumakov, P.M.;
                                          A; Molecule type: DNA
A; Residues: 1-393 <LAM>
                                                                                A; Accession: A25224
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 PWPLSSS--VPSYKTYQGDYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLLSACFRNELVEPRRETP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDGEYFTLKIRGQERFKMFQELNEALELKDAQALKASEDSGAHSSYLKSKKGQSASRLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRNSFEVRICACPGRDRRTEEKNFQKKGEPCPELPPKSAKRALPTNT---SSSPQPKRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDDKQTFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDPSGNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSTPPPGTRVRAMAIYKKLQYMTEVVRRCPHHERSSE-GDG-LAPPQHLIRVEGNMHAEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFLSENV------AGWLEDPGEALQGSAAAAAAPAAEDPVAETPAPVASAPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSST
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                                                                                                         f the human p53 MUID:87064416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 712.5;
                                                                                                                                                                                                                                                                                                                                                                                                                 393
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PMID:2946935
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A; Access type: DNA
A; Molecule type: DNA
A; Rolecule: 1-71, 'P', 73-393 <BUC2>
A; Residues: 1-71, 'P', 73-393 <BUC2>
A; Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID
A; Note: this 72-Pro allele was found in both normal and malignant
A; Note: this 72-Pro allele was found in both normal and malignant
A; Note: this 72-Pro allele was found in both normal and malignant
A; Note: this 72-Pro allele was found in both normal and malignant
A; Note: this 72-Pro allele was found in both normal and malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Molecule type: mRNA
A:Residues: 1-71, pr.,3-272,'H',274-393 <HAR>
A:Residues: 1-71, pr.,3-272,'H',274-393 <HAR>
A:Residues: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
A:Experimental source: clone pR4-2, cell line A431
R:Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.;
Mol. Cell. Biol. 6, 4650-4656, 1986
A:Title: Molecular basis for heterogeneity of the human p53 protein.
A:Reference number: A93086; MUID:87089826; PMID:3025664
A:Accession: A25397
                                                                            A; Molecule type: mRNA; DIA: Residues: 66-79 < MKI3>
                                                                                                                                                                                                                                                                                                                                         A; Title: Primary structure polymorphism at amino acid residue A; Reference number: S42452; MUID:87144273; PMID:3547088 A; Accession: S42452
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-71, 'p', 73-78, 'T', 80-393 <HAR2>
A; Residues: 1-71, 'p', 73-78, 'T', 80-393 <HAR2>
A; Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
A; Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell lin
R; Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford,
Mol. Cell. Biol. 7, 961-963, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-78,'T',80-393 <HAR1>
A;Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
A;Experimental_source: clone p53-H-1, transformed hybridoma SV-80 cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-71,'p','73-393 <ZAK>
A;Reross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
A;Call. Billiamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
R;Harlow, E; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Billiamson, 1601-1610, 1985
A;Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular
A;Reference number: A55060; MUID:85267676; PMID:3894933
A;Accession: A55060
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A; Residues: 101-393 < mKII>
A; Residues: 101-393 < mKII>
A; Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1;
R; Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
EMBO J. 4, 1251-1255, 1985
A; Title: Human p53 cellular tumor antigen: cDNA sequence and e A; Reference number: A22837; MUID:85230577; PMID:4006916
A; Accession: A22837
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                                              A; Experimental source: clone J6K
                                                                                                                                                                                                                          A;Molecule type: mRNA; DNA
A;Residues: 66-71,'p',73-79 <MKI2>
A;Experimental source: clone lambda Cll3
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A; Residues: 1-393 <CHU>
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A; Accession: $40773
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A;NOte: this 72-Arg allele appears to be about 5 times
A;Accession: JT0436
                                                                                                                                                         A; Accession:
                                                                                                                                                                                           A; Note: 72-Cys was also found,
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           Allan,
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       G.J.;
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       Shanahan,
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F.; Vousden,
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                                                                                                                                                                                        represent a
       K.H.;
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       Crook,
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ant cell lines
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EMBO J. 1
A; Title:
                                              A;Molecule type: DNA
A;Residues: 1-393 <FUT>
A;Residues: 1-393 <FUT>
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
A;Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
R;Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi,
Cancer Res. 51, 5800-5805, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-71, p. 73-237, 'Y', 239-393 <F07>
A; Cross-references: EMBL: X60016; NID: g506444;
A; Accession: I38089
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A; Residues: 1-247, 'Q', 249-393 <F06>
A; Cross-references: EMBL:X60015; NID:g506442;
A; Accession: I38088
A; Status: translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
A;Residues: 1-253,'D',255-393 <F11>
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A; Residues: 1-212, 'Q', 214-393 <F10>
A; Cross-references: EMBL: X60019; NID: 9506450;
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A;Residues: 1-247,'Q',249-393 <F08>
A;Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
A;Accession: I38090
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A; Residues: 1-245, 'T', 247-393 <F04>
A; Cross-references: EMBL: X60013; NID: g506438;
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                                                                                                                                                                                                                                                          A; Reference number: A; Accession: 138093
                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 19, 6977, 1991
A;Title: An Alu polymorphism intragenic to the TP53 gene
A;Reference number: I38093; MUID:92107726; PMID:1762941
                                                                                                                                                                                                                                                                                                                                                                                      A;Note: all sequences submitted to the EMBL/GenBank/DDBJR;Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
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A; Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
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A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-236, 'I', 238-393 <F05>
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A; Residues: 1-393 <F03>
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A; Residues: 1-192, 'R', 194-393 <F02>
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A; Accession: I38082
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                                 p53 gene mutations
3 gene mutations in gastric cancer metastases
number: A44905; MUID:92034678; PMID:1933850
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 327-331, 'DQTSFQKENC' <CHO>
A; Residues: 327-331, 'DQTSFQKENC' <CHO>
A; Rossidues: 327-331, 'DQTSFQKENC' <CHO>
A; Rossidues: GR: S66666; NID: g436292; PIDN: AAB28601.1; PID: g436293
A; Note: mutant sequence with altered splicing and termination expressed
R; Petersen, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1959
A; Title: Mapping of linear epitopes recognized by monoclonal antibodies of A; Reference number: S60151; MOID: 96133682; PMID: 8552047
A; Accession: S60153
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A;Title: Alternative splitcing of the p53 tumor suppressor gene A;Reference number: I52681; MUID:94036762; PMID:8221626
A;Accession: I52681
cellular tumor antigen p53 - green monkey (Species: Cercopithecus aethiops (green c.; Species: 10-Sep-1999 #sequence_revision 10 C;Accession: $06594 R;Rigaudy, P.; Eckhart, W.
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J. Biol. Chem. 264, 18019-18023, 1989
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A;Cross-references: GB:S63157; NID:g237829; PIDN:AAB20140.1; PID:g237830
A;Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIP:63158)
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A; Residues: 246-2
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A; Residues: 3-44 < PET>
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                                                                                                                                                                                                                                   NTHGIQMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLEL
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48.9%;
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                                             (green monkey, grivet)
.sion 10-Sep-1999 #text
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C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
C;Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R;Bienz, B; Zakut-Houri, R; Givol, D; Oren, M.
EMBO J. 3, 2179-2183, 1984
                                        A; Molecule type: mRNA
A; Residues: 1-159, 'H, /161-167, 'G', 169-233, 'I', 235-390 <ZAK>
A; Residues: 1-159, 'H, /161-167, 'G', 169-233, 'I', 235-390 <ZAK>
A; Cross-references: GB: X01237; GB: K01700; NID: 953575
A; Arai, N; Nomura, D.; Yokota, K; Wolf, D.; Brill, E.; Sh
Mol. Cell Biol 6, 3232-3239, 1986
                                                                                                                                           A; Reference number: A02684; MUID:84068204; PMID:6646235 A;Accession: A02684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 3, 2179-2183, 1984
A;Title: Analysis of the gene coding for the murine cellular A;Reference number: A22739; MUID:85027173; PMID:6092064
A;Accession: A22739
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A; Title: Immunologically distinct A; Reference number: S38822; MUID:8
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A; Residues: 1-134,'V',
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A; Residues: 1-134,'V',136-390
A; Cross-references: GB: X00876;
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A; Residues: 1-393 < RIG>
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A;Reference number: S06594; M
                                                                                                                                                                                                                                                   R; Zakut-Houri,
                                                                                                                                                                                                                                                                                                                      A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                             A; Accession: S06336
                                                                                                                                                                                                                                                                                                                                                                A; Title: Primary structure of DNA complementary to murine A; Reference number: S06336; MUID:88221682; PMID:3329909
                                                                                                                                                                                                                                                                                                                                                                                                                Bioorg. Khim. 13, 1691-1694, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Chumakov, P.M.
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                                                                                                                                                                                                                                                                      1-134,'V',136-390 <CHU>
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e of a cDNA encoding the monkey
MUID:90045967; PMID:2530498
stinct p53 molecules generated MUID:87064640; PMID:3023970
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; NID:g871420; PIDN:CAA25420.1;
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Pred. No. 1.4e-47;
1; Mismatches 82
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A; ACCESSALU.

A; MOLECULE type: mRNA
A; MOLECULE type: mRNA
A; Residues: 1-167,'G', 169-390 <ARA3>
A; Cross references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1;
A; Cross references: A; Cross references:
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A; Residues: 1-167,'G',169-233,'I',235-390 <ARA2>
A; Cross-references: EMBL:M13873
R; Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, submitted to the EMBL Data Library, July 1988
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F;168-178/Region: conserved region III
F;231-252/Region: conserved region IV
F;233-248/Region: L3 loop
F;267-283/Region: conserved region V
F;313-319/Region: nuclear location signal
F;319-357/Region: tetramer association
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A. Nucleic Acids Res. 12, 5609-5626, 1984
A;Title: Cloning and expression analysis of full length mouse A;Reference number: 148703; MUID:84272240; PMID:6379601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;108-121/Region: L1 loop
F;114-139/Region: conserved region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;16-26/Region: conserved region I
F;99-289/Domain: DNA-binding core #status predicted <DBC>
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A; Residues: 1-47,'R',49-78,'QW',82-390 <RES>
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A; Accession: S40014
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A; Residues: 1-390 < ARA1>
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                                                                                                                                                         LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALELKD---
AHATEESGDSRAHSSYLKTKKGQSTSRHKKTMVK 383
                                                                                                                                                                                                                                                                                                                                                                            NSSCYGGMNRRPILIIVTLETRDGQYLGRRCFEARICACPGRDRKADEDSIRKQQYSDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SREFNEGQ-IAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMC
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                                                                                                                                                                                                                                            KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLP
                                                                                                                                                                                                                                                                                                                                    NSSCMGGMNRRPILTITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEENFRKKEVLCPE
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43.7%; Pred. No. 2.
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                                                                          TYRQQQQQQHQHLLQK 355
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Conservative

60;

Mismatches

32;

Gaps

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A;Gene: p53
C;Superfamil
C;Keywords:
                                                                                                                                                                                                                                                                               R;Lee, H.; Larner, J.M.; Hamlin, J.L. Gene 184, 177-183, 1997
A;Title: Cloning and characterization of Chinese hamster A;Reference number: JC6176; MUID:97183659; PMID:9031625
A;Contents: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor suppressor p53 - rabbit c;Species: Oryctolagus cuniculus (domestic rabbit) c;Date: 11-Apr 1997 #sequence_revision 09-May-1997 #text_C;Accession: JC6193 #s.Le Goas, F.; May, P.; Ronco, P.; de Fromentel, C.C. Gene 185, 169-173, 1997 #species: LONA cloning and immunological characterization A;Reference number: JC6193; MUID:97208869; pMID:9055811 A;Accession: JC6193
                                                                                                                                                         A;Cross-references: GB:U50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230 C;Comment: This protein is a multimer, it plays the central role in a comp iption, and recombination by protein/protein interactions.
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A;Gene: p53
C;Superfamily: cellular
C;Keywords: tumor
                                                                                                                                                                                                                                                                                                                                                                                                        tumor suppressor protein p53 - Chinese C;Species: Cricetulus griseus (Chinese C;Date: 11-Apr-1997 #sequence_revision
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A;Residues: 1-391 <LEA>
A;Cross-references: EMBL:X90592; NID:g1532043;
                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-393 <LEE>
                                                                                                                                                                                                                                                                   A; Accession: JC6176
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                                                                                                                                             ;Genetics:
                                                                                                     Superfamily:
Best Local Signatches 151;
                                          Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TFDAL-SPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQI
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                                                                                                   cellular tumor antigen p53
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Pred. No. 2.4e-47;
                  Score 698; DB 2;
Pred. No. 3.5e-47;
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09-May-1997 #text_change 23-Jul-1999
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                                        Length 393;
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RESULT 12
S38824
cellular tumor a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cellular tumor antigen p53, minor splice form - mouse c;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change C;Accession: S38824; S35478 R;Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, Mol. Cell. Biol. 6, 3232-3239, 1986
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                                                                                                                                       F;267-283/Region: conserved region V
F;313-319/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                  ;319-357/Region: tetramer association
;7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
;7,9,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
;312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status pred.
        Query Match
Best Local Similarity
Matches 139; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LELMQYLPQHTIE-----TYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKGEPCPELPPKSAKRALPTNT---SSSPPPKKKTLDGEYFTLKIRGHERFKMFQELNEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLHSGTAKSVTCTYSPSLNKLFCQLAKTCPVQLWVNSTPPPGTRVRAMAIYKKLQYMTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGVAAAAAST-----AEDPVTETPAPVASAPATPWPLSSS--VPSYKTFQGDYGFRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKES
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          Conservative
                        33.0%;
          49;
      Score 687; DB
Pred. No. 2.4e
49; Mismatches
      DB 2; I
2.4e-46;
hes 81;
                                     Length 381;
      Indels
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      6
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Apporthetical protein K10G6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct
C;Accession: T32008
R;Davidson, S; Wohldmann, P.; Mullen, G.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid K10G6.
A;Reference number: Z21111
A;Accession: T32008
A;Accession: T32008
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1819 < DAV>
A;Cross-references: EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESF
A;Experimental source: strain Bristol N2; clone K10G6
C;Genetics:
A;Gene: CESP:K10G6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The canine p53 gene is subject to somatic mutations A;Reference number: I46226; MUID:95150524; PMID:7847847 A;Accession: I46226
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: I-77 < DEV>
A;Cross-references: GB:L27630; NID:g508454; PIDN:AAC37327.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellular tumor antigen p53 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-Fe
C;Accession: I46226
                                                                                                                                                                                                                                                                      RESULT
T32008
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C; Superfam
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Best Local
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                                                                                                                                                                                                                                                                                                                                                         199 PQVGTEFTTVLYNFMCNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 LPPGSAKRALPTCT---SASPPQKKKPLDGEYFTLKIRGRKRFEMFRELNEALEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 VMCTYSPPLNKLFFQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24/1; 61/3
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                                                                                                                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 60.:
47; Conservative
                                                                                                                                                                                                                                                                                                                                         PEVGFDYTTIHYNYMCNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQDPVTETPGPVA-----PAPATPWPLSSFVPSQKTYQGNYGFHLGFLQSGTAKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellular tumor antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259.5; DB 2
No. 1.1e-13;
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                                                        CESP:K10G6.3
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C;Accession: T42730
R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized A;Reference number: Z22249; MUID:98345363; PMID:9679147
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T42730
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                                                                                                                                                                                                                                                                                                           A;Description: may be involved in cytomatrix organization at the site of neurotransmitte A;Note: component of the presynaptic cytoskeleton C;Keywords: coiled coil; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
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A;Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3942 <DIE>
A;Cross-references: EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g3413810
A;Experimental source: strain 129 SVJ
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 9F1
A;Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bassoon protein - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: bassoon
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                                                                                                                                                                                                                                                                                                                                                                                              ;Function:
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Best Local 9
                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
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                                                                                                                                                                                                                                     Local Similarity
                                                                                                2110 LNSMDQYGGRHGSGSGGPDLVQYQPQHGP-GLSAPQGLAPLRSGLLGNPTYPEGQPS--- 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1057 HHHQQQHHQ-----QNQQQAPGNRSRSHSNV 1082
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                                                                                                                                                  23 LNSMDQQ-IQNGSSSTSP----YNTDHAQNSVTAPSPYAQPSS-----TFDALSPSPAI 71
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PGNLAQYGPAASQATAVRQLLPSTATVRAADGMIYST----INTPIAATLPITTQPASVL 222:
                                     PSNTDYPGPHSFDVSFQQSSTAKSAT-----WTYSTELKKLYCQIAKTCPIQIK---VM 122
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                     5.2%; Score 109; DE 21.6%; Pred. No. 16; tive 57; Mismatches
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Search completed: August 7, 2003, 09:53:31
Job time: 14.3901 secs

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Nature 400:792-792(1999).
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[8]
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Kharbanda S., Weichselbaum R., Kufe D.;

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[9]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99380160; PubMed=10449409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The emerging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Cancer Inst. 91:594-598(1999).
DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN NEUROBLASTOMA AND OLICODENDROGLIOMA.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                         TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCE INDUCTION: NOT INDUCED BY DAMAGE.

DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DON TO THE ABL TYROSINE KINASE SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPIC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM D INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE
                                                                                                                                                                                                                                                 Name=Kappa;
IsoId=015350-7;
                                                                                                                                                                                                                                                                                                                                                                                                      Name=Epsilon;
IsoId=O15350-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                 IsoId=015350-5; Sequence=VSP_006544, Note=The splicing of exon 11 results original reading frame. The splicing reading frame to the sequence of isof
                                                                                                                                                                                                                                                                                          IsoId=015350-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           original reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note=The splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=015350-3; sequence=VSP_006540,
Note=The splicing of exon 11 results
                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=015350-4; Sequence=VSP_006542,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=015350-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=015350-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shioya H., Ishiko T., Sun X., Weichselbaum R., Kufe D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p53 gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: Nuclear.
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                                                                                                                                                                                                                                                 Sequence=VSP_006538;
                                                                                                                                                                                                                                                                                        Sequence=VSP_006546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence=VSP_006539
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of exon 13
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in a frameshift
                                                                                                                                                                                                                                                                                                                                                                                                                                             VSP_006543;
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in a frameshift
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Pfam; PF00870; P53; 1.
Pfam; PF00536; SAM; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
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                              VARSPLIC
                                                                                                                                                                           Transcription regulation;
Apoptosis; Nuclear protein
                                                                                                                                                                                                                                                          GO; GO:0006298; P:mismatch repair; InterPro; IPR002117; P53. InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                             GO; GO:0003700; F:transcription factor activity; TAS. GO; GO:0008630; P:induction of apoptosis by DNA damage; GO; GO:0006298; P:mismatch repair; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an
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                                                          VARSPLIC
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AF0776.16

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Y11416; CAA72221.
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HGNC:12003; TP73.
                                                                                                                                                                                                  PS00348; P53;
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n; Phosphorylation; Alternative splicin
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د.
         QYRMTIWRGLQDLKQGHDYSTAQQLLRSSNAATISIGGSGE
LQRQRVMEAVHFRVRHTITIPNRGGPGGGPDEWADFGFDLP
                            isoform Kappa).
/FTId=VSP_006538.
SFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPE
                                                                   BETA)
                                                                                                                    ASP/GLU-RICH (ACIDIC).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MEDIATES OLIGOMERIZATION (POTENTIAL).
POLY-PRO.
                                                                             PHOSPHORYLATION
                                                                                       DNA-BINDING
                                                                                                 POLY-PRO
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                                                                                                                                                           TRANSACTIVATION
                                                          GNTRCRHWVLCGDRGLSRPVLQGPSG
                                                                                       (POTENTIAL).
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Best I
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
28-FEB-2003 (Rel. 4
Tumor protein p73 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P73_CERAE
Q9XSK8; Q9
                          between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: PARTICIPATES IN THE APOPYGOTIC RESPONSE TO DNA DAMAGE.

- WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN (BY SIMILARITY).

-1- SUBJUIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABLUTROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
Cercopithecinae; Cercopithecus.
NCBI_TaxID-9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caput D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                ISOId-Q9XSK8-2; Sequence-VSP_006537;
DOMAIN: POSSESES AN ACIDIC TRANSACTIVATION DOMAI
BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION
TO THE ABL TYROSINE KINASE SH3 DOMAIN.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                          AND WITH P53, WHEREAS ISOFORM SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
ween the Swiss Institute of Bioinform
European Bioinformatics Institute. To
by non-profit institutions as long
                                                                                                                                                                                                                                                                             Event=Alternative Name=Alpha;
                                                                                                                                                                                                                                    Name=Beta;
                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186
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38; Conservative
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Apoptosis; Nuclear protein
VARSPLIC 495
                                                                                                                                           Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Onco
SEQUENCE FROM N.A.
MEDLINE-92210006; PubMed-1339362;
de Fromentel C.C., Padkel F., Cha
"Rainbow trout p53: cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y11419; CAA72224.1;
EMBL; Y11419; CAA72225.1;
HSSP; O15350; 1COK.
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ProDom; PD002081; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
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                                                                                                                       NCBI_TaxID=8022;
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n; Phosphorylation; Alternative splicing.
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QYRMTIMRGLQDLKQGHDYGAAAQQLLRSSNAAAISIGGSG
ELQRQRVMEAVHFRVRHTITIPNRGGPGAGPDEWADRGFDL
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PRINTS; PR00386; P53SUPPRESSR.

ProDom; PD002681; P53; 1.

PROSITE; PS00348; P53; 1.

Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis.
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European Bioinformatics Institute. There are no restrictions
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SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
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NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
8422250765545A1C CRC64;
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MBL outstation -
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                                  VLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRK
                                                                                                                               KRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTT
                VLYNFMCNSSCMGGMNRRPILTIISLETHDGQLLGRRSFEVRVCACPGRDRKTEESNFRK
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                                                                                                                                                                          PQSGTAKSVTCTYSSDLNKLFCQLAKTCPVQMVVNVAPPQGSVIRATAIYKKSEHVAEVV
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Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
"Evolutionary conservancy of p53 gene sequences in fish.";
"Evolutionary conservancy of p53 gene sequences in fish.";
"Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.

Apoptosis induction seems to be mediated either by stimulation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barbus barbus (Barbel).
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; 'Cyprinidae; Barbus.
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16-OCT-2001 (Rel. 40, I
28-FEB-2003 (Rel. 41, I
Cellular tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF071570; AAD34212.1; HSSP; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nuclear protein; Phosphorylation; Apoptosis
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InterPro; IPR002117; P53.
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SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
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QQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVV
                                                                     ELINDEYLPSSFDPNIFDNVLTEQPQPSTSP-----PTASVPVATDYPGEHGFKLGF
                                                                                                                     QIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSF
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40, Last sequence update)
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tigen p53 (Tumor suppressor p53).
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                                                                                                                                                                                                Score 819.5;
Pred. No. 2.
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NUCLEAR LOCALIZATION SIGNAL (POTE
PHOSPHORYLATION (BY SIMILARITY).
; OBEZCFZCEA74C304 CRC64;
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BY SIMILARITY.
OLIGOMERIZATION.
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Teleostei; Ostariophysi; Cypriniformes;
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P79734; Q90440;
01-NOV-1997 (Re
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DOMAIN
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                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
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                                                                      DOMAIN
                                                                                 Nuclear protein; Phosphorylation;
                                                                                              Anti-oncogene; DNA-binding; Transcription
                                                                                                           ProDom; PD002681; P53; PROSITE; PS00348; P53;
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                                                                                                                                                                                                                                                                                                                                                              expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
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BAX and FAS antigen
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Chordata; Craniata; Vertebrata; Eu
pterygii; Teleostei; Ostariophysi;
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           BASIC (REPRESSION OF DNA-BINDING) NUCLEAR LOCALIZATION SIGNAL (POTE
                                         BY SIMILARITY. OLIGOMERIZATION.
                                                     cion; Apoptosis.
TRANSCRIPTION ACTIVATION
BY SIMILARITY.
 PHOSPHORYLATION
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SIMILARITY)
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093379;
                                                                        This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=99071979; PubMed=9854815;

Luft J.C., Bengten E., Clem L.W., Miller N.W.,

Luft J.C., Bengten E., Clem L.W., Miller N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euxaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Tictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ictalurus punctatus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                           modified and
                                                                                                                                                                                                                                                                                                                                     Comp
                                                                                                                                                                                                                                                                                                                                                      channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                     "Identification and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                       expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                     FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                     BAX and FAS antigen expression, or by repression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 LRPEGSKKAKGSSSDEEIFTLQVRGRERYEILKKLNDSLELSDVVPASDAEKYRQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
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                                                                                                                                                                                                                                                                                                                                     Biochem. Physiol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ENNAQTQFSEPQYTNL----
                                                                                                                                                                                                                                                                                                                                     catfish (Ictalurus punctatus).";
iochem. Physiol. 120B:675-682(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRV
                                         non-profit institutions as long and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETQEGQLLGRRSFEVRVCACPGRDRKTEESNFKKDQETKTMAKTTTGTKRSLVKESSSAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGNQRANYREDNITLRHSVFVPYEAPQLGAEWTTVLLNYMCNSSCMGGMNRRPILTIITL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCPVQMVVDVAPPQGSVVRATAIYKKSEHVAEVVRRCPHHE--RTPDGDNLAPAGHLIRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQ
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Pred. No. 2.8
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                                                         There are no rest
ong as its content
                                                                                                                                                                                                                                                                                                                                                                     the tumor suppressor
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                                              and
                                                                                             EMBL
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                                              for
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                                                                                                         collaboration
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SEQUENCE
SEQUENCE FROM N.A.
MEDLINE-94134403; PubMed-8302570;
Hoever M., Clement J.H., Wedlich i
"Overexpression of wild-type p53
in Xenopus laevis embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1988 (Rel. 07,
01-APR-1988 (Rel. 07,
28-FEB-2003 (Rel. 41,
                                                                                                                                  "Cloning and characterization of a cDNA from for a protein homologous to human and murine Oncogene 1:71-78(1987).
                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                           Cellular
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                                                                                                                                                                                                                         MEDLINE=88143684; PubMed=2830576;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                Xenopodinae;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 800; DB 1; Pred. No. 8.9e-54;
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1B89CD98DB3289F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362
                         interferes
                      Montenarh M., Knoechel W.; erferes with normal develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                  May P.,
                                                                                                                                                                                                                                                                                                                                  Pipoidea;
                                                                                                                                                       Xenopus p53.";
                                                                                                                                                                                                                                                                                                                                                                                                                       p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 376;
                      normal development
                                                                                                                                                                                                  Kress M.;
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                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                             laevis
                                                                                                                                                                                                                                                                                                                                  Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
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CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M36962; AAA49923.1; -. EMBL; X05191; CAA28821.1; -. EMBL; X77546; CAA54672.1; -. CCCCR. AAC60746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 9:109-120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S68353; AAC60746.1;
PIR; A29376; A29376.
HSSP; P04637; LTUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: Binds DNA as a homotetramer (
-i- SUBCELLULAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: Ubiquitous.
-i- SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                    Local Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression (By similarity).
SUBUNIT: Binds DNA as a homotetramer (By similarity).
SUBCELLULAR LOCATION: Nuclear.
                                                                                                               187
                                                                                                                                          188
298
                            302
                                                      247
                                                                                 248
                                                                                                                                                                       128
                                                                                                                                                                                                  128
                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00386; P53SUPPRESSR.
                                                                                                                           GRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILLIVTLETRDGQVLGRRCFE 247
                                                                                                                                                                                   GAVIRAMPYYKKAEHYTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPIT 187
DDEEIFTLRIKGRSRYEMIKKLNDALELQESLDQQKV
                                                      VRVCACPGRDRRTEEDNYTKKRGLKPSGK
                                                                                                                                                                                                                                             SPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQ
                          PDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTI
                                                                                ARICACPGRDRKADEDS-IRKQQVSDSTKNGDGTKRPFRQNTH--GIQMTSIKKRR---S
                                                                                                               GRHSVCVPYEGPQVGTECTTVLYNYMCNSSCMGGMNRRPILTIITLETPQGLLLGRRCFE
                                                                                                                                                                       GSILRATAVYKKSEHVAEVVKRCPHHERSVEPGE-DAAPPSHLMRVEGNLQAYYMEDVNS
                                                                                                                                                                                                                             SCAVPSTDDYAGKYGLQLDFQQNGTAKSVTCTYSPELNKLFCQLAKTCPLLVRVESPPPR
                                                                                                                                                                                                                                                                                                                                                                          76
300
344
281
362
52
71
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Apoptosis.
29 TRANSCRIPTION ACTIVATION
267 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                           267
331
356
293
362
52
71
                                                                                                                                                                                                                                                                                                                                              40692 MW;
                                                                                                                                                                                                                                                                                                   36.6%;
54.5%;
                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription regulation;
                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY SIMILARITY).
7 -> S (IN REF. 2).
MISSING (IN REF. 2).
MISSING (IN REF. 2).;
CELF3E58F020D74D CRC64;
                                                                                                                                                                                                                                                                                    Score 762; DB 1;
Pred. No. 6.7e-51
2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                  BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                              OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                       68;
                            338
                                                                                                                                                                                                                                                                                                                Length
                                                        RELAHPPSSEPPLPKKRLVVVD
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                                                                                                                                                                                                                                                                                                                  363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            induces
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                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 16:11383-11383(1988).
-!- FUNCTION: Acts as a tumor suppressor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Archosauria; Aves; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P53_CHICK
                                                                                                                                                                                                                              ProDom;
                                                                                                                                                                                                                                             InterPro; IPR002117; p53. Pfam; pF00870; p53; 1.
                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                              oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-SPAFAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989
                                                                                                                                 SEQUENCE
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                Nuclear protein;
                                                                                                                                                                                                                   ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                           PIR; S02193; S02193.
                                                                                                                                                                                                                                                                                    EMBL; X13057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence of a cDNA encoding the oncoprotein ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89083584; PubMed=3060861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
                                                                                                                                                               DOMAIN
                                                                                                                                                                                DNA_BIND
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                            Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                          growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity)
                                                                                                                                           RES
                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                    119
                                      108
                                                                                                                                                                                                                                                                 P04637; 1TUP
 168
                                                         61
                                                                          48
                                                                                                      Similarity
                                                                                                                                                                                                                                      PR00386; P53SUPPRESSR.
                              YCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPP
                                                                         SVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKL 107
SHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPI 227
                  YCRLAKPCPVQVRVGVAPPPGSSLRAVAVYKKSEHVAEVVRRCPHHERCGGGTDG-LAPA
                                                                                                                               87
308
347
292
366
367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel.
                                                                                             Conservative
                                                                                                                                                                                                                                                                                     CAA31456.1;
                                                                                                                                 AA;
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339
364
306
306
40169
                                                                                                                                                                                                Phosphorylation; Apoptosis
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10, Last
41, Last
tigen p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasiani
                                                                                                    36.4%;
                                                       -TPPRAAPSPVVPSTEDYGGDFDFRVGFVEAGTAKSVTCTYSPVLNKV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update) annotation update)
                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Tumor suppressor
                                                                                                                                                                                                         Transcription regulation;
                                                                                                      Pred.
                                                                                                           Score 758.5;
                                                                                                                                        BASIC (REPRESSION OF DNA-BINDING).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                     TRANSCRIPTION ACTIVATION BY SIMILARITY. OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                FC37D0FCDF9195B6 CRC64;
                                                                                            Mismatches
                                                                                                     No. 1.3e-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                               http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tebrata; Euteleostomi;
Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53).
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                                                                                            Indels
                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p53
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                                                                                                                                                                                                          Activator;
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DOMAIN
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                       Oncogene
                                                                                                                                                                                                                                                                                                                                                                                       antibodies."
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9TUB2;
16-OCT-2001
                                                       DOMAIN
                                                                                 PROSITE;
                                                                                                               Pfam; PF00870; P53;
                                                                                                                       InterPro; IPR002117;
                                                                                                                                HSSP; P04637; 1C26
                                                                                                                                         EMBL;
                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P53_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286
                                                                                PD002681; P53; PS00348; P53;
                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumor antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel.
         94
318
361
304
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41,
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or send an email to license@isb-sib.ch).
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WEDLINE-99422034; PubMed-10490836;
BUXT P.D., Argyle D.J., Reid S.W.J., Nasir L.;
"Nucleotide sequence of the porcine p53 cDNA, and
"Nucleotide sequence n53 expressed in vitro with a
                                                                                                                                                                     Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation a trans-activator that acts to negatively regulate cell divisior by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation o BAX and FAS antigen expression, or by repression of BCl-2
                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
ified and this statement is not removed. Usage by an
ities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Binds DNA as SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: p53 is found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                           AF098067; AAF04620.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEASE: p53 is found in increased amounts in a transformed cells. p53 is frequently mutated
                                                                                                                                                                                                                                              PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDG--TKRPFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQ
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Phosphorylation; Apoptosis.

45
TRANSCRIPTION ACTIVATION (ACIDIC)
285
BY SIMILARITY.
349
OLIGOMERIZATION.
380
BASIC (REPRESSION OF DNA-BINDING)
316
NUCLEAR LOCALIZATION SIGNAL (POTE
15
PHOSPHORYLATION (BY PRPK) (BY
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P41685;
01-NOV-1995 (Rel. 32, Cr
01-NOV-1995 (Rel. 32, La
28-FEB-2003 (Rel. 41, La
Cellular tumor antigen p
TP53 OR TRP53.
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
NCBI_TaxID=9685;
                                                                                                                                                                           "Molecular cloning and chromosomal mapping suppressor gene.";
J. Vet. Med. Sci. 55:801-805(1993).
                                                                                                                                                                                                                                                        O'Brien S.J., Tsujimoto H., Hasegawa A.;
                                                                                                                                                                                                                                                                                Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watari T.,
                                                                                                                                                                                                                                                                                                        SEQUENCE OF 34-354 FROM N.A. MEDLINE-94114699; Pubmed-8286534;
                                                                                                                                                                                                                                                                                                                                                                                                               hematopoietic
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Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y.,
Watari T., Goitsuka R., Tsujimoto H., Hasegawa A.;
"Cloning of feline p53 tumor-suppressor gene and it
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                     FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved the capture of cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases.
     Apoptosis
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                                                                                                                                                                                                 RESULT 11
P53_BOVIN
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CONFLICT
SEQUENCE
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taurus
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Query Match
Best Local S
Matches 147
                                                 P53_BOVIN
Q29628;
Q1-NOV-1997
Q1-NOV-1997
28-FEB-2003
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                Cellular tumor antigen p53 TP53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-oncogene; DNA-binding; Trans
Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00870; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D26608; BAA0
EMBL; D16460; BAA0
HSSP; P04637; 10LG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Binds DNA as SUBCELLULAR LOCATION: DISEASE: p53 is found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in many types of cancer.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear. DISEASE: p53 is found in incre of transformed cells. p53 is f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAX and FAS antigen expression, expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
147; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00386; P53SUPPRESSR.
                                                                                                                                                                                                                                                                                                  NSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDST
                                                                                                                                                                                                                                                                                                                                                                          SATWITYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHE
                                                                                                                                                                                                             PPPGSTKRALPPST - - - SSTPPQKKKPLDGEYFTLQIRGRERFEMFRELNEALEL
                                                                                                                                                                                                                                             KNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLEL
                                                                                                                                                                                                                                                                                                                                                       RCPDSSDG-LAPPQHLIRVEGNLHAKYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNFMC
                                                                                                                                                                                                                                                                                                                                                                                                                         SYTCTYSPPLNKLFCQLAKTCPVQLWVRSPPPPGTCVRAMAIYKKSEFMTEVVRRCPHHE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDASGMSAVPAPAAPAPAT----PAPAISWPLSSFVPSQKTYPGAYGFHLGFLQSGTAK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHAQNSVTAPSPYAQPSSTFDALSPSPAI-----PSNTDYPGPHSFDVSFQQSSTAK 94
                                                                                                                                                                                                                                                                                   NSSCMGGMNRRPIITIITLEDSNGKLLGRNSFEVRVCACPGRDRRTEEENFRKKGEPCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385
285
386
(Bovine),
                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
318
361
304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAA03927.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385
285
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349
380
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
                                  (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation; Activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 753.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        × ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tion; Apoptosis.
TRANSCRIPTION ACTIVATION (ACIDIC)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASIC (REPRESSION OF DNA-BINDING). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIGOMERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           increased
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D08B43BA1BC8EB78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       frequently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or by
                                                                                                                       386
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ently mutated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wide variety or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                               343
                                                                                                                                                                                                                                                                                                                                                                                          214
                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
                                                                                                                                                                                                                                                                                   291
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishop R.R.P., Gobright E.E.I.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAS antigen expression, or by repression of Bcl-2
                                                         MOD_RES
CONFLICT
                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dequiedt F., Kettmann R., Burny A., Willems L.; "Nucleotide sequence of the bovine P53 tumor-suppressor cDNA."; DNA Seq. 5:261-264(1995).
                                                                                                                                                                                                                    PRINTS; PR00386; P53SUPPRESSR
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.; "Predominant p53 mutations in enzootic bovine leukemic cell lines."; yet. Immunol. Immunopathol. 52:53-63(1996).
                                           SEQUENCE
                                                                                                                                               DOMAIN
                                                                                                                                                            DNA_BIND
                                                                                                                                                                                                        Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-B.indicus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-Bovine; STRAIN-Holstein; MEDLINE-96401400; PubMed-8807776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 13-386 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95352829; PubMed-7626789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Bovine; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria
Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos indicus (Zebu).
                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISEASE: p53 is found of transformed ~~1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression.
SUBUNIT: Binds DNA as
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                         5; U74486; AAB51214.1; S51648; S51648.
9; P04637; 1TUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE P53 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in many types of cancer
                                                                                                                                                                                                                                                              Pro; IPR002117; P53. PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                    X81704; CAA57348.1; -. D49825; BAA08629.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transformed cells, p53 is frequently mutated or
                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
                                          380
386 AA;
                                                                                                    94
318
361
304
                                                                                                                                                                                                 DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9915;
                                                                                                                                                                         Phosphorylation; Apoptosis.

44 TRANSCRIPTION ACTIVATION
                                                                                                    285
349
380
316
15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cetartiodactyla; Ruminantia; Pecora;
                                           43255
35.8%;
41.7%;
                                           ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a homotetramer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in increased amounts in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear.
Score
Pred.
                                                         Ħ
                                                                                                                 BASIC (REPRESSION OF NUCLEAR LOCALIZATION
                                                                    PHOSPHORYLATION (BY SIMILARITY)
                                                                                                  PHOSPHORYLATION (BY
                                                                                                                                               OLIGOMERIZATION
                                                                                                                                                            BY SIMILARITY
                                           222473F28C548F31
                                                         -> T (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Thymus
745.5; DB 1
No. 1.3e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                         as its content
             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                           CRC64;
                                                                                                    PRPK)
                                                                                                                   SIGNAL (POTE
            Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wide variety or inactivated
                                                                                                                                                                         (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovoidea;
                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                             commercia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P53_TETMU
Q9W679;
           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                          Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.; "Evolutionary conservancy of p53 gene sequences in fish."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon miurus (Congo puffer).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; Eu
Acanthomorpha; Acanthopterygii; Percomorph
Tetraodontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cellular tumor antigen p53 (Tumor suppressor p53).
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TP53 OR P53
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=94908;
                                                                                                                                                     expression (By similarity).
SUBUNIT: Binds DNA as a homote
SUBCELLULAR LOCATION: NUClear.
SIMILARITY: BELONGS TO THE P53
                                                                                                                                                                                                                                            FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                            BAX and FAS antigen expression, or by repression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 YRQQQQQQH-QHLLQKHLLS-ACFRNELVEPRRETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 PSLNKLFCQLAKTCPVQLWVDSPPPPGTRVRAMAIYKKLEHMTEVVRRCPHHERSSDYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 ---SPYAQPSSTFDALSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPFRQNTHGIQMTSIKKRRSP-DDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNRRPILTITLEDSCGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGQSCPEPPPRSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-LAPPQHLIRVEGNLRAEYLDDRNTFRHSVVVPYESPEIDSECTTIHYNFMCNSSCMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPSAPAAPPPAT----PAPATSWPLSSFYPSQKTYPGNYGFRLGFLQSGTAKSVTCTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELNVEPPLSQETFSDLWNLLPENNLLSSELSAPVDDLLPYTDVATWLDECPNE--APQMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENNAQTQFSEPQYTNLGLL----NSMDQQIQNGSSSTSPYN-----TDHAQNSVTAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RALPTNT----SSSPQPKKKPLDGEYFTLQIRGFKRYEMFRELNDALEL-----KDALDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67;
                                                                                                                                                                                            homotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                          P53 FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                             (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei
rpha; Tetraodontiformes;
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                                                                                                                                                                                            similarity).
                                                Usage
                                                               its content
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                                                                                   restrictions
                                                  and
                                                                                                    EMBL
                                                                                                                                                                                                                               Bc1-2
                                                                     18
                                                                                                        a collaboration
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                                                  ior
                                                                                                  outstation
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P53_CAP

P53_CAP

ID P53_C

AC Q2953

DT 01-NC

DT 15-DE

DT 28-FE

DT 28-FE

DT CELLU

GN TP53

OC EUKAI

OC Manuna

OX NCBI_

RN [1]

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P53_CANFA STANDANA,
P53_CANFA STANDANA,
Q29537; Q9TV78;
Q1-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update).
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                             Setoguchi A., Sakai T., Okuda M., Mir
Setoguchi A., Sakai T., Okuda M., Mir
Watari T., Hasagawa A., Tsujimoto H.;
"Aberrations of p53 tumor suppressor
                                             Submitted
                                                                                                                                                                                                                Veldhoen N., Milner J.;
"Isolation of canine p53 cDNA and full length canine p53 protein.";
Oncogene 16:1077-1084(1998).
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nuclear protein; Phosphorylation; DOMAIN 1 47 TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD002681; P53; 1
PROSITE; PS00348; P53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPROUP Pfam; PF00870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF071571; AAD34213.1; HSSP; P04637; ITUP.
  SEQUENCE
                                                                    tumors in
                                                                                                                                                 TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                      TISSUE=Leukocyte;
MEDLINE=98178696;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00386; P53SUPPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297
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148; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKSKTASSAEEDNNEVYTLQIRGRKRYEMLKKINDGLDLLENKPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPPSRDGANSSSPTVPVTTDYPGEYGFKLRFQKSGTAKSVTSTYSEILNKLYCQLAKTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGIVLGRRCFEVRVCACPGRDRKTEETNSTKMQ-----
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                                           (DEC-1998) to the
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342
288
  25-300
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                                                                                                                                                                                                                                                                                                        PubMed=9519881;
FROM
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337
363
301
                                                                                                                                                                                                                                                                                                                                                                                                                 Carnivora; Fissipedia;
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51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                               hordata; Craniata; Vertebrata;
arnivora; Fissipedia; Canidae;
  z
                                                                                                        Okuđa M., Minehata K., Tsujimoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Mismatches
                                        EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 745; Db 1,
No. 1.3e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLIGOMERIZATION
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                                                                                   gene in
                                                                                                                                                                                                                                                             characterization
                                                                                   various
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                                                                                                                            Yazawa M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                 Canis.
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                                                                                                                              Ishizaka
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD002681; P53; PROSITE; PS00348; P53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04637; 10LG.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF060514; AAC16909.1; -.
EMBL; AB020761; BAA78379.1; -.
EMBL; S77819; AAB42022.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-oncogene; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95323915; PubMed=7600529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Beagle;
                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of BC1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in many types of cancer. SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression.
SUBUNIT: Binds DNA as a homotetramer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuc
DISEASE: p53 is found in
                               193
                                                                                           134
                                                             181
                                                                                                                       121
                                                                                                                                                                                                                                                                         153;
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                                                                                                                                                                                                                                           J
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00386; P53SUPPRESSR.
                                                                                                                                                   PL----SSSVPSPKTYPGTYGFRLGFLHSGTAKSVTWTYSPLLNKLFCQLAKTCPVQLW
                                                                                                                                                                               TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                               YLDDRNTFRHSVVVPYEPPEVGSDYTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNV
                                             YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                         VSSPPPPNTCVRAMAIYKKSEFVTEVVRRCPHHERCSDSSDG-LAPPQHLIRVEGNLRAK
                                                                                                                     VMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ
                                                                                                                                                                                                                                           ENNAQTQFSEPQYTNL----GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                             ENNVLSSELCPAVDELLLPESVVNWLDE-----DSDDAPRMP--ATSAPTAPGP--APSW
                                                                                                                                                                                                                                                                                                                                     381 AA;
                                                                                                                                                                                                                                                                                                                                                    378
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313
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299
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                              380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation;
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                                                                                                                                                                                                                                                                                       35.5%;
                                                                                                                                                                                                                                                                                                                                     MW;
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                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription
                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                     Score 739;
                                                                                                                                                                                                                                                                                                                                                 L -> P
                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY SIMILARITY).
MEES -> MQEP (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY PRPK) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                        BASIC (REPRESSION OF DNA-BINDING)
NUCLEAR LOCALIZATION SIGNAL (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OLIGOMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSCRIPTION ACTIVATION (ACIDIC).
                                                                                                                                                                                                                                                                                                                                     761A718FDC93DA59 CRC64;
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis
                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                    (IN REF. 2).
                                                                                                                                                                                                                                                                                       4e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region
                                                                                                                                                                                                                                                                                                     DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulation;
                                                                                                                                                                                                                                                                           102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of exons 3-8.";
                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P53_ORYLA STANDARD; PRT; 352 AA. P79820; Q9PSU7; Q9PSU8; Q1-NOV-1997 (Rel. 35, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor;
                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinfornmatics and the EMBL outsit the European Bioinfornmatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contenting the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P "Isolation of cDNAs encoding the p53 tumor suppressor Japanese Medaka (Oryzias latipes).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krause M.K., Rhodes L.D., van Beneden R.J.;
"Cloning of the p53 tumor suppressor gene from (Oryzlas latipes) and evaluation of mutational exposed fish.";
Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.

DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 87 273 BY SIMILARITY.
                                                                       PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Japanese Medaka (Oryzias latipes).";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                             Pfam; PF00870; P53;
                                                                                                                                              InterPro; IPR002117; P53.
                                                                                                                                                                                                                    EMBL; U57306; AAC60146.1; -.
                                                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                                                            entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TP53 OR P53.
                                                                                                                                                                                                                                                                                                                                                                                                  expression (By similarity).
SUBUNIT: BINGS DNA as a homotetramer (By
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAX and FAS antigen expression, or by repression
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                                                                                                                                                               AF003949; AAD01195.1; -. AF003950; AAD01196.1; -. P04637; 1YCS.
                                                                                                                                                                                                                                                       s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND VARIANT THR-91.
                                                                                                                                                                                                                                                                        (See
                                                                                                                                                                                                                                                                   http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the Japanese medaka hotspots in MNNG-
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RESULT 15
P53_MAC
P53_MO
D7 16-0C
D7 16-0C
D7 28-FE
D8 4753.
OS MARIMO
OC ELLIU
GN 7953.
OS MARIMO
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Best Local :
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                       MEDITINE=97376996; PubMed=9233767; Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.; "Partial characterization of the woodchuck tumor suppressor, its interaction with woodchuck hepatitis virus x antigen in hepatocarcinogenesis."; Oncogene 15:327-336(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Cellular tumor antigen p53 (Tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    036006;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marmota monax (Woodchuck).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marmota.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                       in many types of cancer.
SIMILARITY: BELONGS TO THE P53
                                                                                           SUBUNIT: Binds DNA as a homotetramer SUBCELLULAR LOCATION: Nuclear. DISEASE: p53 is found in increased am of transformed cells. p53 is frequent in many types of cancer.
                                                                                                                                                                                                                                growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2
                                                                                                                                                                                                                 expression
                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Acts as a tumor suppressor
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Rodentia;
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52.5%;
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MISSING (IN REF. 1).
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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Sciurognathi;
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thi; Sciuridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ001022; CAA04478.1; HSSP; P04637; 1TUP. InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein;
                                                                                                                                                                                                                              al Similarity 41.5%; Score 736.5; DB 1 159; Conservative 63. Minmath.
                                                                                                                311 SSSPQPKKKPLDGEYFTLKIRGRARFEMFQELNEALELKDAQAEK--
                                                                                                                                292 QMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQH 351
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                                                                                                                                                                                       237 DGQVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNT-----HGI 291
                                                                                                                                                                                                                                                                                                                      117
                                                         366 YLKSKKGQSTSRHKKIIFKREGP 388
                                                                                   352 LLOKHLLSACFRNELVEPRRETP 374
                                                                                                                                                                                                                                                                                        141 VQLWVDSTPPPGTRVRAMAIYKKSQHMTEVVRRCPHHE--RCSDSDGLAPPQHLIRVEGN
                                                                                                                                                                                                                                                                                                                                                                  65 LSPSPA-----IPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCP 116
                                                                                                                                                                                                                                                                                                                                                  81 AAPSPATSWPLSSSVPSQNTYPGVYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQLAKTCP
                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                                                                                                                       IQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGN 176
                                                                                                                                                                                                                                                                                                                                                                                                          ENNVLSPVLSPPMDDL-LLSSED--VENWFDK----GPDEALQMSAAPAPKAPTPAASTL
                                                                                                                                                                        SGNLLGRNSFEVRVCACPGRDRRTEEENFRKR-----GEPCPEPPPRSTKRALPNGT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390
391 AA;
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323
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44 TRANSCRIPTION ACTIVATION (ACIDIC).
290 BY SIMILARITY.
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             7, 2003, 09:47:30
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ElDE5DB84Ba40182 CRC64;
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb;
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_rotent:
12: sp_vtrus:*
13: sp_vtrus:*
14: sp_unclass
15: sp_vtrus:
16: sp_bacteri
17: sp_archeap
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Gapop 10.0 , Gapext 0.5
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2082
1 MLYLENNAQTQFSEPQYTNL.....PKQSDVFFRHSKPPNRSVYP 393
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sp_bacteria:*
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SUMMARIES

Result	Score	% Query Match	Length	DB	Ħ	Description
_	2082	100.0	393	4	075922	075922 homo sapien
2	2039	97.9	393	11	Q99JD9	Q99jd9 rattus norv
ω	2011	96.6	487	4	Q9H3D2	Q9h3d2 homo sapien
4	2009	96.5	389	11	668880	O88899 mus musculu
ហ	1973	94.8	470	11	Q99JE1	
6	1973	94.8	487	11	Q99JE0	· Q99je0 rattus norv
7	1938	93.1	483	11	088897	
8	1884	90.5	416	4	Q9P1B6	homo
9	1884	90.5	461	4	Q9P1B5	homo
. 10	1884	90.5	461	4	Q9UP26	•
11	1884	90.5	586	4	Q9UBV9	homo
12	1884	90.5	586	4	Q9P1B4	homo
13	1882	90.4	461	11	Q9QWY9	9 mus
14	1882	90.4	586	11	089097	mus
15	1873	90.0	461	11	299лр6	ratt
16	1873	90.0	586	11	099ле2	rattus

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31'	30	29	28	27	26	25	24	23	22	21	20	19	18	17
1085.5				1256.5	1268	1268	1272	1381.5	1489	1551.5	1551.5	1591.5	1722	1807	1807	1807	1807	1808	1811	1811	1813	1813	1813	1813	1813	1813	1867	8
						60.9	61.1	66.4	71.5	74.5	74.5	76.4	82.7	86.8	86.8	86.8	86.8	86.8	87.0	87.0	87.1	87.1	87.1	87.1	87.1	87.1	89.7	89.7
514	232	587	450	426	641	631	590	501	284	588	576	457	365	089	663	555	538	582	680	555	680	680	641	555	516	471	586	356
11	4	4	4	4	13	11				13			13	11	11	11	11	13	11	11		-	-	4	4	4	4	4
Q9CU77	Q96KR0	Q8TDY6	Q8TDY5	Q8NHW9	Q9W664	Q9JJP2	Q9JJP1	Q9Н3Р8	Q8C826	Q8JHZ6	Q8JFE3	Q8JHZ5	Q98SW0	Q9JJP6	099ЛЕЗ	Q99JD8	Q99JD7	· Q9DEC7	868880	Q9QWZ0	Q9UE10	Q9H3D4	075195	Q9H3D3	Q9P1B7	Q9NPH7	075080	Q9UP74
7 mus	pomo	Q8tdy6 homo sapien	homo	Omo	Q9w664 barbus barb	Q9jjp2 mus musculu	Q9jjp1 mus musculu	Q9h3p8 homo sapien					Q98sw0 xenopus lae	Q9jjp6 rattus norv	Q99je3 rattus norv	Q99jd8 rattus norv	rattus	Q9dec7 gallus gall	mus mu	mus	Q9uel0 homo sapien	homo						

ALIGNMENTS

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THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.	A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION	GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL	-!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES	Submitted (TAN-1999) to the FMRI/ConBank/DDBI databases	FROM N.A.	[3]	Mol. Cell 2:305-316(1998).	ninant-negative ac	"p63, a p53 homolog at 3g27-29, encodes multiple products with	Andrews N.C., Caput D., McKeon F.;		MEDITAREGRA/AROOS. DIPMONEGRATO/AROO.	CECHTOLOG GEOV N	(a) MeObidata 1:11-12(1222).	"Mutation and expression of the p51 gene in human lung cancer.";	Yokota J.;	Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,	MEDLINE=20388515; PubMed=10935472;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	O.	Homo sapiens (Human).		·	soform DELNGAMMA (DN P6	OCT-2002	(TrEMBLrel. 08,	01-NOV-1998 (TremBLrel. 08, Created)	075922;	O75922 PRELIMINARY; PRT; 393 AA.	LT 1 22

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EMBL; AF116759; AAF43490.1; JU
EMBL; AF116760; AAF43490.1; JU
EMBL; AF116761; AAF43490.1; JU
EMBL; AF116762; AAF43490.1; JU
EMBL; AF116763; AAF43490.1; JU
EMBL; AF116763; AAF43490.1; JU
EMBL; AF116765; AAF43490.1; JU
EMBL; AF116765; AAF43490.1; JU
EMBL; AF124540; AAG43612.1; JU
EMBL; AF124540; AAG43612.1; JU
EMBL; AF124531; AAG43612.1; JU
EMBL; AF124532; AAG43612.1; JU
EMBL; AF124534; AAG43612.1; JU
EMBL; AF124534; AAG43612.1; JU
EMBL; AF124534; AAG43612.1; JU
EMBL; AF124535; AAG43612.1; JU
EMBL; AF124535; AAG43612.1; JU
EMBL; AF124535; AAG43612.1; JU
EMBL; AF124536; AAG45612.1; JU

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: BINDS DNA AS A NUCLEAR (BY SIMILARITY) SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY) DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED MANY TYPES OF CANCER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFORMED CELLS. P53 IS FREQU
MANY TYPES OF CANCER (BY SIMILA
SIMILARITY: BELONGS TO THE P53
L; AF075429; AAC62634.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXPRESSION (BY SIMILARITY)
                                                                                                                                            361
                                                                                                                                                                                                                                                        241
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                                                                                                            361
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AF116758; AAF43490.1;
AF116759; AAF43490.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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AND FAS ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                             CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
                                                                                                                                                                                                                                                                           LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                                             YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                                              TEDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                        CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
                                                                                                                                                                                                   SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
                                                                                                                                                                              SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
                                                                                                                                                                                                                                                      LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                                                                                                                                                                                                            YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEEMS TO BE MEDIATED EITHER BY STIMULATION EXPRESSION, OR BY REPRESSION OF BCL-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2082; DB 4;
Pred. No. 3.7e-178;
                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                  393
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                                                                                                                                            393
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
             CFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
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C. -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES C GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CELL CYCLE REGULATION AS A TEAMS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES: REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. C APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).

C -!- SUBGUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).

C -!- SUBGULLUAR LOCATION: NUCLEAR (BY SIMILARITY).

C -!- SUBGULLUAR LOCATION: NUCLEAR (BY SIMILARITY).

C -!- SUBGULLUAR LOCATION: NUCLEAR (BY SIMILARITY).

C -!- SIMILARITY: BELONGS TO THE PS3 FAMILY.

DR MANY TYPES OF CANCER (BY SIMILARITY).

C -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR MANY TYPES OF CANCER (BY SIMILARITY).

DR HSSP; P04637; 1YCS.

DR HSSP; P04637; 1YCS.

DR FAMIL PRO02117; P53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TIEMBLEEL 1 01-JUN-2001 (TIEMBLEEL 1 01-OCT-2002 (TIEMBLEEL 2 01-OCT-2002 (TIEMBLEEL (Cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269; Bamberger C., Schmale H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear Phosphorylation; Transcription; Transcription regulation. SEQUENCE 393 AA; 44471 MW; 1A310CA62CB276DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; PP0002681; P53; 1.
PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 501:121-126(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification and tissue distribution
                                                                                                                                                                                                                                                                                 TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
                                                                                                                                                                                                               MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQQHQHLLQKHLLSA
                  SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLLQKHLLSA
                                                                    LGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRR
                                                                                                                                            YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                             YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                                                                                                                                                                                                                                                                        MLYLESNAQTQFSEPQYTNLGLLNGMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           97.9%;
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Pred. No. 2.7e
1; Mismatches
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                              2.7e-174;
ches 7;
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ion update)
igen p53).
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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361

CFRNELVESRREAPTQSDVFFRHSNPPNHSVYP 393

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RESULT

OCCUPANT

OCCUPANT
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01-MAR-2001
01-OCT-2002
                  Pfam; PF00870; P53; 1.
Pfam; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
Protom: P500348; P53; 1.
                                                                                                                                                                                                               EMBL;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9H3D2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osada M., Ohba M., Kawahara C., Ishioka C., Ikawa Y., Nimura Y., Nakagawara A., Obinata Ikawa Y., Nimura Y., Nakagawara Ohinata Ikawa Y., Ishioka C., Ishioka Ishioka C., Ishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Skeletal muscle;
MEDLINE-98324755; PubMed-9662378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tani M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 40-487 MEDLINE=20388515; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              functionally resembles p53."
Nat. Med. 4:839-843(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF
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SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                              AF116770; AAF43486.1
AF116756; AAF43486.1
AF116757; AAF43486.1
AF116759; AAF43486.1
AF116760; AAF43486.1
AF116761; AAF43486.1
AF116762; AAF43486.1
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AF124534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF124531;
AF124532;
                                                                                                                                                                                                                                            AF116763; AAF43486
AF116764; AAF43486
AF116765; AAF43486
                                                                                                                                                                                                                   P04637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF124529;
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-2001 (TrEMBLrel. 16, Last sequence up
-2002 (TrEMBLrel. 22, Last anotation
gamma (P51 isoform TAP63GAMMA).
       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         076078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimizu K., Kawahara C.,
                                                                                                                                             IPR002117; P53.
0870; P53; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and expression of the 1:71-79(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40-487 FROM N.A.
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BAA32592.
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PubMed=10935472;
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Best Local
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088899;
01-NOV-1998
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01-OCT-2002
  EMBL;
HSSP;
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                                                                                                                                                                                                                                                                                                                      Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                         TRP63.
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                                                                                                                                                                                                         transactivating, death-inducing, and Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                     *p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death inducing, and dominant-negative activit;
                                                                                                                                                                                                                                                       MEDLINE-98448095; PubMed-9774969; Yang A., Kaghad M., Gillett E., Fleming
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
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EXPRESSION (BY SIMILARITY).

SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).

SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN I
TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OF
MANY TYPES OF CANCER (BY SIMILARITY).

SIMILARITY: BELONGS TO THE P53 FAMILY.

SIMILARITY: AC62642.1; -.

SP; P04637; 1YCS.
                                                                                                        FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375
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                                                                                                                                                                                                                                                                                                                   Eutheria;
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Rodentia;
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Pred. No. 1.1e-171;
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ED OR INACTIVATED
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Best Local S
Matches 382
                    -I- SUBCELLULAR LOCATION: NUCLEAR
-I- SIMILARITY: BELONGS TO THE PE
EMBL; AJAZ77448; CAC37100.1; -.
HSSP; P04637; 1YCS;
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOm; PD002681; P53; 1.
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Q99JE1;
                                                                                                                                                                          variants.";
FEBS Lett. 501:121-126(2001).
rocation: NUCLEAR
                                                                                                                                                                                                                                                                    STRAIN=Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed=11470269; Bamberger C., Schmale H.;
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01-JUN-2001 (TrEMBLrel.
01-CCT-2002 (TrEMBLrel.
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ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
PROSITE; PS00348; P53; 1.
Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear Phosphorylation; Transcription; Transcription regulation.
SEQUENCE 389 AA; 43970 MW; FE6B4A859C5F00BB CRC64;
      PROSITE;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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InterPro; IPR002117; P53.
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22,
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Last annotation update)
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Pred. No. 1.3e-171;
0; Mismatches 7;
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Sciurognathi; Muridae;
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Best Local Sin
Matches 372;
                    Query Match
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Best Local
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Q99JE0;
Q1-JUN-2001
01-JUN-2001
01-OCT-2002
                                                  PRINTS; PR00386; P538UPPRESSR.
ProDom; PD002881; P53; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
                                                                                                              -!- SUBCELLULAR LOCATION: NUCLEAR I-!- SIMILARITY: BELONGS TO THE P53 EMBL; AJ277449; CGC37101.1; -. HSSP; P04637; 1YCS.
                                                                                                                                                                                    STRAIN-Wistar; TISSUE-Tongue; MEDLINE-21363378; PubMed-11470269; Bamberger C., Schmale H.;
                                                                                           HSSP; P04637; 1YCS.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                          Nuclear protein. SEQUENCE 487 F
                                                                                                                                                        FEBS Lett.
                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                  variants.";
                                                                                                                                                                           Bamberger C., Schmale H.;
"Identification and tissue distribution
                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                                                                        501:121-126(2001).
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  Conservative
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98.2%;
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Last annotation update)
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Pred. No. 2.8e
0; Mismatches
Score 1973; DB 11;
Pred. No. 2.9e-168;
D; Mismatches 7;
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Sciurognathi; Muridae;
                                          A688F392F32B3039
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FAMILY.
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es 7;
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                                          CRC64;
                    Length
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                      487;
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Neoplasia 1:71-79(1999).

CIPCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOGIS DEPENDING ON THE PHYSIOLOGICAL GROWTH ARREST OR APOPTOGIS DEPENDING ON THE PHYSIOLOGICAL GROWTH ARREST OR APOPTOGIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTRANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE ORD OF THE ACTIVATED GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

CHAPPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).

CHORDOLOGY.

CHAPTORY OF THE PHYSIOLOGY.

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INDUCTION SEEMS TO NEGATIVE AND THE PHYSIOLOGY.

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A TRANSFORMED CELLS. PS3 IS FREQUENTLY MUTATED OR INACTIVATED IN
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                                          GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mutation and expression of the p51 gene in human lung cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE-20388515; PubMed-10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update P51 isoform delNdelta (Cellular tumor antigen p53) Homo sapiens (Human).
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-!- SIMILARITY: BELONGS TO THE P53 FAMILY.

EMBL, AF116769; AAF43493.1; -.

EMBL, AF116759; AAF43493.1; JOINED.

EMBL, AF116760; AAF43493.1; JOINED.

EMBL, AF116761; AAF43493.1; JOINED.

EMBL, AF116762; AAF43493.1; JOINED.

EMBL, AF116764; AAF43493.1; JOINED.

EMBL, AF116764; AAF43493.1; JOINED.

EMBL, AF116764; AAF43493.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                TQSDVFFRHSNPPNHSVYP 483
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Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
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EMBL; AF116766; AAF43493.1;
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                                                                                       TDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAVIRAM 134
                                                                                                                                                                           PVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
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74
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MEDLINE-98488095; PubMed-9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
Caput D., McKeon F.,
                                                                                                              ETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVEPRRETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQYTNLGLLNSMDQQ1QNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPA1PSN
                                                                                                                                                                                                                                                                   PYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACP
                                                                                                                                                                                                                                                                                                                                                          GRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGR
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-i- SUBCELDUAR LOCATION: NUCLEAR (BY SIMILARITY).

-i- SIMILARITY: BELONGS TO THE P53 FAMILY.

EMBL; AF075434; AAC62639.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Last sequence update)
Last annotation update)
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InterPro; IPR002117; P53.
Pfam; PF00870; P53; IPRINTS; PR00386; P53SUPPRESSR.
ProDom; PD002681; P53; DPROSITE; PS00348; P53; 1.
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SEQUENCE 483 1
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TRP63.
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Best Local S
Matches 368
15
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AF124533; AAG45611.1;
AF124534; AAG45611.1;
AF124535; AAG45611.1;
                                                     461 AA; 51305
ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
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                                     Nuclear protein
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Q9UP26;
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EMBL;
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Matches
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                                                                                                                                                            1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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                                                                                                           Gaps
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| "Mutation and expression of the p51 gene in human lung cancer.";
| Neoplasia 1:71-79(1999).
| Substitution and Location | NUCLEAR (BY SIMILARITY).
| SINGLIARITY: BELONGS TO THE P53 FAMILY.
| EMBL, AF116769; AAF43492.1; JOINED. |
| REMBL, AF116769; AAF43492.1; JOINED. |
| REMBL, AF116761; AAF43492.1; JOINED. |
| REMBL, AF116762; AAF43492.1; JOINED. |
| REMBL, AF116763; AAF43492.1; JOINED. |
| REMBL, AF116764; AAF43492.1; JOINED. |
| REMBL, AF116765, AAF43492.1; JOINED. |
| REMBL, AAF43492.1; JOINED. |
| R
Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein; Phosphorylation; Transcription; Transcription regulation. SEQUENCE 416 AA; 46589 WW; A5974A14B25E3118 CRC64;
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BEDLINE-20388515; PubMed=10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          16;
                                                                        Length 416;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                    90.5%; Score 1884; DB 4;
93.3%; Pred. No. 2.2e-160;
live 3; Mismatches 7;
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EMBL; AF116766; AAF43492.1; JOINED.
EMBL; AF116767; AAF43492.1; JOINED.
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Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
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                                                                                     Best Local Similarity 93.3
Matches 361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                      Query Match
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Q9P1B5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                181 YVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQV
                                                                                                       Gaps
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Yang.A., Raghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                               16;
                                                Length 461;
                                                                                                    Indels
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Submitted (JAN-1999) to the EmbL/Genbank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
68B63547B81C1B05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                              Score 1884; DB 4;
Pred. No. 2.6e-160;
3; Mismatches 7;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last anno
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EMBL; AF124539; AAG45611.1;
EMBL; AF124530; AAG45611.1; JOINED.
EMBL; AF124531; AAG45611.1; JOINED.
EMBL; AF124531; AAG45611.1; JOINED.
     MM:
                                              y Match 90.5%;
Local Similarity 93.3%;
les 361; Conservative
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DR DR DR KW

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TFDALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 SPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSA 360
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2002 (TrEMBLrel. 22, Last annotation update)
p51 isoform delNalpha.
PFI thoo sapiens (Human).
Eukaryota: Metazona; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherta; Primates; Catarrhin; Hominidee; Homo.
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                                                             Hagiwara K., McMenamin M.G., Harris C.C.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE P53 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2E2F92ABF1AF8629 CRC64;
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                                                                                                                                                                EMBL, AF075431, AAC626361; EMBL, AF091627; AAC43038.1; EMBL, AF124539, AAC45610.1; CHEBL; AF124539, AAC45610.1; CHEBL; AF124531, AAC45610.1; CHEBL; AF124531, AAC45610.1; JOINED. EMBL, AF124532, AAC45610.1; JOINED. EMBL, AF124535, AAC45610.1; JOINED. EMBL, AF124535; AAC45610.1; JOINED. EMBL, AF124535; AAC45610.1; JOINED. EMBL, AF124536; AAC45610.1; JOINED. EMBL, AF124538; AAC45610.1; JOINED.
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InterPro; IPR00117; P53.
InterPro; IPR001660; SAM.
Pfam; PR00870; P53; I.
PRINTS; PR00386; P53SUPPRESSR.
ProDom; P0002081; P33; I.
SMART; SM00454; SAM; I.
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Matches 361; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLYLENNAQTQFSEPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS
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MEDIATR=94848095; PubMed-9774969;
WEDIATR=94848095; PubMed-9774969;
Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
Andrews N.C., Caput D., McKeon F.;
"p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
Mol. Cell 2:305-316(1998).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Dellavalle R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,
Jablonska S.;
                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                  Length 461;
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Last annotation update)
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93.3%; Pred. No. 2.6e-160;
tive 3; Mismatches 7;
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EMBL; AF124536; AAG45611.1; JOINED. EMBL; AF124537; AAG45611.1; JOINED. HSSP; PO4637; 1YCS. InterPro; IPR002117; P53. Pfam; PF00870; P53; 1.
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                                                                                                                                      PRINTS; PR00386; P53SUPPRESSR. ProDom; PD002681; P53; 1. PROSITE; PS00348; P53; 1.
                                                                                                                                                                                                                                                       461 AA; 51404 MW;
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Matches 361; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                         | Muration and expression of the p51 gene in human lung cancer.";
| Neoplasia 1:71-79(1999).
| SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
| SIMECRILORS TO THE P53 FAMILY.
| REBE: AF116758; AAF43491.1; JOINED.
| REBE: AF116759; AAF43491.1; JOINED.
| REBE: AF116760; AAF43491.1; JOINED.
| REBE: AF116761; AAF43491.1; JOINED.
| REBE: AF116762; AAF43491.1; JOINED.
| REBE: AF116763; AAF43491.1; JOINED.
| REBE: AF116764; AAF43491.1; JOINED.
| REBE: AF116764; AAF43491.1; JOINED.
| REBE: AF116764; AAF43491.1; JOINED.
| REBE: AF116765; AAF43491.1; JOINED.
                                         ŠEČUENCE FROM N.A.
BEDLINE-20388515; Pubmed-10935472;
Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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PRINTS, PRO0386; P53SUPRESSR.
Probom; PD002681; P53; 1.
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EMBL; AF116767; AAF43491.1;
EMBL; AF116768; AAF43491.1;
HSSP; P04637; 1VC
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InterPro; IPR001660; SAM.
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PROSITE; PS00348; P53; 1.
Nuclear protein.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
                                                                                                        MEDLINE-98448095; PubWed-9774969;
Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews
Caput D., McKeon F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                             461 AA; 51455 MW; 7613296F2F85DBC8 CRC64;
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93.0%; Pred. No. 3.9e-160;
11ve 3; Mismatches 8;
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01-OCT-2002 (TrEMBLrel.
DN P63 alpha.
TRP63 OR P73H.
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SEQUENCE 461 P
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A Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachib A Fanoaka T., Shinkai Y., Kato H.;
A Tanaka T., Shinkai Y., Kato H.;
A Fanoaka T., Shinkai Y., Kato H.;
T "A second p53-related protein, p73L, with high homology to Biochem. Blophys. Res. Commun. 248:603-607(1998).
C -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
C -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
R EMBL; AF075439; AAC62644.1; -.
R EMBL; AF075439; AAC62644.1; -.
R EMBL; AB010152; BAA32432.1; -.
R HSSP; P04637; IYCS.
R MGD; MGI:1330810; Trp63.
R InterPro; IPR001660; SAM.
R Pfam; PF00870; P53; 1.
Q99JD6;
01-JUN-2001
01-JUN-2001
01-OCT-2002
DN KET beta
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Yang A., Kaghad M., Gillett E., Fleming M.D.,
Caput D., McKeon F.;
"p63, a p53 homolog at and the processing transfer."
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ProDom; PD002681; P53; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00348; P53; 1.
Nuclear protein.
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Best Loc
Matches
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-!- SUBCELLULAR LOCATION: NUC-
-!- SINILARITY: BELONGS TO TH-
EMBL; AJZ77453; CAC37105.1; -
HSSP; P04637; 1YCS.
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Mammalia; Eutheria;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and tissue distribution of variants.";
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Rattus norvegicus (Rat).
Craniata; Vertebrata; Euteleostomi;
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4; Mismatches
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